

Sequence Listing

<110> Baker, Kevin P.
 Botstein, David
 Desnoyers, Luc
 Eaton, Dan L.
 Ferrara, Napoleone
 Fong, Sherman
 Gao, Wei-Qiang
 Goddard, Audrey
 Godowski, Paul J.
 Grimaldi, Christopher J.
 Gurney, Austin L.
 Hillan, Kenneth J.
 Pan, James
 Paoni, Nicholas F.
 Roy, Margaret Ann
 Smith, Victoria
 Stewart, Timothy A.
 Tumas, Daniel
 Watanabe, Colin K.
 Williams, P. Mickey
 Wood, William I.

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 Cys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val Asp Thr Gln Gln
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 50 55 60
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
 65 70 75
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
 80 85 90
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
 95 100 105

Asp His Trp Lys	Ala Leu Ala Phe Arg	Leu Glu Glu Glu Gln Lys	110	115	120
Met Arg Pro Glu	Ile Ala Gly Leu Lys	Pro Ala Asn Pro Pro Val	125	130	135
Leu Pro Ala Pro	Gln Lys Ala Asp Thr	Asp Pro Glu Asn Leu Pro	140	145	150
Glu Ile Ser Ser	Gln Lys Thr Gln Arg	His Ile Gln Arg Gly Pro	155	160	165
Pro His Leu Gln	Ile Arg Pro Pro Ser	Gln Asp Leu Lys Asp Gly	170	175	180
Thr Gln Glu Glu	Ala Thr Lys Arg Gln	Glu Ala Pro Val Asp Pro	185	190	195
Arg Pro Glu Gly	Asp Pro Gln Arg Thr	Val Ile Ser Trp Arg Gly	200	205	210
Ala Val Ile Glu	Pro Glu Gln Gly Thr	Glu Leu Pro Ser Arg Arg	215	220	225
Ala Glu Val Pro	Thr Lys Pro Pro Leu	Pro Pro Ala Arg Thr Gln	230	235	240
Gly Thr Pro Val	His Leu Asn Tyr Arg	Gln Lys Gly Val Ile Asp	245	250	255
Val Phe Leu His	Ala Trp Lys Gly Tyr	Arg Lys Phe Ala Trp Gly	260	265	270
His Asp Glu Leu	Lys Pro Val Ser Arg	Ser Phe Ser Glu Trp Phe	275	280	285
Gly Leu Gly Leu	Thr Leu Ile Asp Ala	Leu Asp Thr Met Trp Ile	290	295	300
Leu Gly Leu Arg	Lys Glu Phe Glu Glu	Ala Arg Lys Trp Val Ser	305	310	315
Lys Lys Leu His	Phe Glu Lys Asp Val	Asp Val Asn Leu Phe Glu	320	325	330
Ser Thr Ile Arg	Ile Leu Gly Gly Leu	Leu Ser Ala Tyr His Leu	335	340	345
Ser Gly Asp Ser	Leu Phe Leu Arg Lys	Ala Glu Asp Phe Gly Asn	350	355	360
Arg Leu Met Pro	Ala Phe Arg Thr Pro	Ser Lys Ile Pro Tyr Ser	365	370	375
Asp Val Asn Ile	Gly Thr Gly Val Ala	His Pro Pro Arg Trp Thr	380	385	390
Ser Asp Ser Thr	Val Ala Glu Val Thr	Ser Ile Gln Leu Glu Phe			

395	400	405
Arg Glu Leu Ser	Arg Leu Thr Gly Asp Lys Lys Phe Gln Glu Ala	
410	415	420
Val Glu Lys Val	Thr Gln His Ile His Gly Leu Ser Gly Lys Lys	
425	430	435
Asp Gly Leu Val	Pro Met Phe Ile Asn Thr His Ser Gly Leu Phe	
440	445	450
Thr His Leu Gly	Val Phe Thr Leu Gly Ala Arg Ala Asp Ser Tyr	
455	460	465
Tyr Glu Tyr Leu	Leu Lys Gln Trp Ile Gln Gly Gly Lys Gln Glu	
470	475	480
Thr Gln Leu Leu	Glu Asp Tyr Val Glu Ala Ile Glu Gly Val Arg	
485	490	495
Thr His Leu Leu	Arg His Ser Glu Pro Ser Lys Leu Thr Phe Val	
500	505	510
Gly Glu Leu Ala	His Gly Arg Phe Ser Ala Lys Met Asp His Leu	
515	520	525
Val Cys Phe Leu	Pro Gly Thr Leu Ala Leu Gly Val Tyr His Gly	
530	535	540
Leu Pro Ala Ser	His Met Glu Leu Ala Gln Glu Leu Met Glu Thr	
545	550	555
Cys Tyr Gln Met	Asn Arg Gln Met Glu Thr Gly Leu Ser Pro Glu	
560	565	570
Ile Val His Phe	Asn Leu Tyr Pro Gln Pro Gly Arg Arg Asp Val	
575	580	585
Glu Val Lys Pro	Ala Asp Arg His Asn Leu Leu Arg Pro Glu Thr	
590	595	600
Val Glu Ser Leu	Phe Tyr Leu Tyr Arg Val Thr Gly Asp Arg Lys	
605	610	615
Tyr Gln Asp Trp	Gly Trp Glu Ile Leu Gln Ser Phe Ser Arg Phe	
620	625	630
Thr Arg Val Pro	Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val Gln	
635	640	645
Asp Pro Gln Lys	Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe	
650	655	660
Leu Gly Glu Thr	Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp	
665	670	675
Pro Asn Leu Leu	Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala	
680	685	690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
ggcgccgcgt aggcccgga ggccgggccc gccgggctgc gagcgccctgc 50
cccattgcgc gccgcctctc cgcacgatgt tcccctcgcg gaggaagcg 100
gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150
ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gctttctctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtcg ggggacaagg gcaggagacc tcggggccctc cccgtgcctg 300
 cccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350
 cccaccgcct ggcagtgctg gtgcccttcc gcgaacgctt cgaggagctc 400
 ctggtcttcg tgccccacat gcgcccgttc ctgagcagga agaagatccg 450
 gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500
 cagcgtcat caacgtgggc ttcttgaga gcagcaacag cacggactac 550
 attgccatgc acgacgttga cctgctccct ctcaacgagg agctggacta 600
 tggttttctt gaggtgggc ccttcacgt ggcctccccg gagctccacc 650
 ctctctacca ctacaagacc tatgtcggcg gcatcctgct gctctccaag 700
 cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggctgggg 750
 ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800
 ttttcgccc ctcgggaatc acaactgggt acaagacatt tcgccacctg 850
 catgaccag cctggcgga gagggaccag aagcgcatcg cagctcaaaa 900
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 accatgtggc ttcccgact gccctgtctg tgggcggggc cccctgcact 1000
 gtctcaaca tcatgttga ctgtgacaag accgccacac cctggtgcac 1050
 attcagctga gctggatgga cagtaggaa gcctgtacct acaggccata 1100
 ttgctcaggc tcaggacaag gcctcaggtc gtgggcccag ctctgacagg 1150
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 ggccgccaag gcaggcttgg gctgggccag gacacgtggg gtgcctggga 1250
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 cccaggcctg tgggtagtgg ggagggctga acaggacaac ctctcatcac 1400
 cctactctga cctccttcac gtgccaggc ctgtgggtag tggggagggc 1450
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 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
 <211> 327
 <212> PRT
 <213> Homo sapiens
 <220>

<221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 19-25,65-71,247-253,285-291,303-310
 <223> N-myristoylation site.

<220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

<400> 17
 Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp
 1 5 10 15
 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
 20 25 30
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
 35 40 45
 Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
 50 55 60
 Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
 65 70 75
 Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
 80 85 90
 Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
 95 100 105
 Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
 110 115 120
 Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
 125 130 135
 His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

Glu	Ser	Ser	Asn	Ser	Thr	Asp	Tyr	Ile	Ala	Met	His	Asp	Val	Asp
				155					160					165
Leu	Leu	Pro	Leu	Asn	Glu	Glu	Leu	Asp	Tyr	Gly	Phe	Pro	Glu	Ala
				170					175					180
Gly	Pro	Phe	His	Val	Ala	Ser	Pro	Glu	Leu	His	Pro	Leu	Tyr	His
				185					190					195
Tyr	Lys	Thr	Tyr	Val	Gly	Gly	Ile	Leu	Leu	Leu	Ser	Lys	Gln	His
				200					205					210
Tyr	Arg	Leu	Cys	Asn	Gly	Met	Ser	Asn	Arg	Phe	Trp	Gly	Trp	Gly
				215					220					225
Arg	Glu	Asp	Asp	Glu	Phe	Tyr	Arg	Arg	Ile	Lys	Gly	Ala	Gly	Leu
				230					235					240
Gln	Leu	Phe	Arg	Pro	Ser	Gly	Ile	Thr	Thr	Gly	Tyr	Lys	Thr	Phe
				245					250					255
Arg	His	Leu	His	Asp	Pro	Ala	Trp	Arg	Lys	Arg	Asp	Gln	Lys	Arg
				260					265					270
Ile	Ala	Ala	Gln	Lys	Gln	Glu	Gln	Phe	Lys	Val	Asp	Arg	Glu	Gly
				275					280					285
Gly	Leu	Asn	Thr	Val	Lys	Tyr	His	Val	Ala	Ser	Arg	Thr	Ala	Leu
				290					295					300
Ser	Val	Gly	Gly	Ala	Pro	Cys	Thr	Val	Leu	Asn	Ile	Met	Leu	Asp
				305					310					315
Cys	Asp	Lys	Thr	Ala	Thr	Pro	Trp	Cys	Thr	Phe	Ser			
				320					325					

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 18
 gcgaacgctt cgaggagtc tgg 23

<210> 19
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-24
<223> Synthetic construct

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 20
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100
gactggctgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150
gattgggcct tctttccccc ttcctttctg tgtctcctgc ctcatcggcc 200
tgccatgacc tgcagccaag ccagccccc tggggaaggg gagaaagtgg 250
gggatggcta agaaagctgg gagatagga acagaagagg gtagtgggtg 300
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tottatacta 350
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450
taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

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Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly
  1           5           10           15
Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
          20           25           30
Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
          35           40           45
Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
          50           55           60
Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
          65           70
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<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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gggacccatg cggccgtgac ccccggtccc ctagaggccc agcgcagccg 50
cagcggacaa aggagcatgt ccgcgccggg gaaggcccgt cctccggccg 100
ccataagggt cgggtcgccg ctggggcccgc gccgcgctcc tgcccggccg 150
ggctccgggg cggcccgccta ggccagtgcg ccgccgctcg ccccgcaggc 200
cccgggcccgc agcatggagc caccgggacg ccggcggggc cgcgcgcagc 250
cgccgctggt gctgccgctc tcgctgttag cgctgctcgc gctgctggga 300
ggcggcgggc gcgggcggcg cgcggcgctg cccgccggct gcaagcacga 350
tgggcgggcc cgaggggctg gcagggcggc gggcgccgcc gagggcaagg 400
tggtgtgcag cagcctggaa ctgcgcagg tcctgcccc agatactctg 450
cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500
gaagaatggc tcattttctg ggttaagtct cttgaaaga ttggacctcc 550
gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600
tctctaaaaa gattggtatc gacaaacaat cgaataggat gtctgaatgc 650
agacatattt cgaggactca ccaatctggt tcggctaaac ctttcgggga 700
at ttgttttc ttcattatct caaggaactt ttgattatct tgcgtcatta 750
cggctcttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800
gtggatgcat cgctgggtaa aggagaagaa catcacggta cgggatacca 850
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ggtgtgttta	tcctaagtca	ctgcaggccc	aaccagtcac	aggcgtgaag	900
caggagctgt	tgacatgcga	ccctccgctt	gaattgccgt	ctttctacat	950
gactccatct	catcgccaag	ttgtgtttga	aggagacagc	cttcctttcc	1000
agtgcattggc	ttcatatatt	gatcaggaca	tgcaagtgtt	gtggtatcag	1050
gatgggagaa	tagttgaaac	cgatgaatcg	caaggatatt	ttgttgaaaa	1100
gaacatgatt	cacaactgct	ccttgattgc	aagtgcccta	accattttcta	1150
atattcaggc	tggatctact	ggaaattggg	gctgtcatgt	ccagacccaa	1200
cgtgggaata	atacgaggac	tgtggatatt	gtggtattag	agagttctgc	1250
acagtactgt	cctccagaga	gggtggtaaa	caacaaaggt	gacttcagat	1300
ggcccagAAC	attggcaggc	attactgcat	atctgcagtg	tacgcggaac	1350
acccatggca	gtgggatata	tcccggaaac	ccacaggatg	agagaaaagc	1400
ttggcgcaga	tgtgatagag	gtggcttttg	ggcagatgat	gattattctc	1450
gctgtcagta	tgcaaatgat	gtcactagag	ttctttatat	gtttaatcag	1500
atgcccctca	atcttaccAA	tgccgtggca	acagctcgac	agttactggc	1550
ttacactgtg	gaagcagcca	acttttctga	caaaatggat	gttatatttg	1600
tggcagaaat	gattgaaaaa	tttggaagat	ttaccaagga	ggaaaaatca	1650
aaagagctag	gtgacgtgat	ggttgacatt	gcaagtaaca	tcatgttggc	1700
tgatgaacgt	gtcctgtggc	tggcgcagag	ggaagctaaa	gcctgcagta	1750
ggattgtgca	gtgtcttcag	cgcattgcta	cctaccggct	agccggtgga	1800
gctcacgttt	attcaacata	ttcacccaat	attgctctgg	aagcttatgt	1850
catcaagtct	actggcttca	cggggatgac	ctgtaccgtg	ttccagaaaag	1900
tggcagcctc	tgatcgtaca	ggactttcgg	attatgggag	gcgggatcca	1950
gagggaaacc	tggataagca	gctgagcttt	aagtgcaatg	tttcaaatac	2000
attttcgagt	ctggcactaa	aggtatgtta	cattctgcaa	tcatttaaga	2050
ctattttacag	ttaaattaga	atgctccaaa	tgttctgctt	cgcaaaataa	2100
ccttattaaa	agattttttt	ttgcagggaag	ataggtatta	ttgctttttgc	2150
tactgtttta	aagaaaacta	accaggaaga	actgcattac	gactttcaag	2200
ggccctaggc	atttttgcct	ttgattccct	ttcttcacat	aaaaatatca	2250
gaaattacat	tttataactg	cagtggata	aatgcaaata	tactattggt	2300

acatgtgaaa aaatittatt tgacttaaaa gtttatttat ttgttttttt 2350
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 atgagccttt ggcaactgcg ctgccaagcc tagtggagaa gtcaaccctg 2450
 agaccaggtg tttaatcaag caagctgtat atcaaaattt ttggcagaaa 2500
 acacaaatat gtcatatatc tttttttaaa aaaagtattt cattgaagca 2550
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 atttgactac actgtattga agcaaataga ggaggcacaa ctccagcacc 2650
 ctaatggaac cacatttttt tcacttagct ttctgtgggc atgtgtaatt 2700
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 ctgatccaac aggtgttagg tgttctggtt tagtgtgagc actcaataaa 2850
 tattgaatga atgaacgaaa aaaaaaaaaa aaa 2883

<210> 24
 <211> 616
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-33
 <223> Signal peptide.

<220>
 <221> TRANSMEM
 <222> 13-40
 <223> Transmembrane domain (type II).

<400> 24
 Met Glu Pro Pro Gly Arg Arg Arg Gly Arg Ala Gln Pro Pro Leu
 1 5 10 15
 Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly
 20 25 30
 Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His
 35 40 45
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
 50 55 60
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
 65 70 75
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
 80 85 90

Asn Lys Ile Ser	Glu Leu Lys Asn Gly Ser Phe Ser Gly Leu Ser	95	100	105
Leu Leu Glu Arg	Leu Asp Leu Arg Asn Asn Leu Ile Ser Ser Ile	110	115	120
Asp Pro Gly Ala	Phe Trp Gly Leu Ser Ser Leu Lys Arg Leu Asp	125	130	135
Leu Thr Asn Asn	Arg Ile Gly Cys Leu Asn Ala Asp Ile Phe Arg	140	145	150
Gly Leu Thr Asn	Leu Val Arg Leu Asn Leu Ser Gly Asn Leu Phe	155	160	165
Ser Ser Leu Ser	Gln Gly Thr Phe Asp Tyr Leu Ala Ser Leu Arg	170	175	180
Ser Leu Glu Phe	Gln Thr Glu Tyr Leu Leu Cys Asp Cys Asn Ile	185	190	195
Leu Trp Met His	Arg Trp Val Lys Glu Lys Asn Ile Thr Val Arg	200	205	210
Asp Thr Arg Cys	Val Tyr Pro Lys Ser Leu Gln Ala Gln Pro Val	215	220	225
Thr Gly Val Lys	Gln Glu Leu Leu Thr Cys Asp Pro Pro Leu Glu	230	235	240
Leu Pro Ser Phe	Tyr Met Thr Pro Ser His Arg Gln Val Val Phe	245	250	255
Glu Gly Asp Ser	Leu Pro Phe Gln Cys Met Ala Ser Tyr Ile Asp	260	265	270
Gln Asp Met Gln	Val Leu Trp Tyr Gln Asp Gly Arg Ile Val Glu	275	280	285
Thr Asp Glu Ser	Gln Gly Ile Phe Val Glu Lys Asn Met Ile His	290	295	300
Asn Cys Ser Leu	Ile Ala Ser Ala Leu Thr Ile Ser Asn Ile Gln	305	310	315
Ala Gly Ser Thr	Gly Asn Trp Gly Cys His Val Gln Thr Lys Arg	320	325	330
Gly Asn Asn Thr	Arg Thr Val Asp Ile Val Val Leu Glu Ser Ser	335	340	345
Ala Gln Tyr Cys	Pro Pro Glu Arg Val Val Asn Asn Lys Gly Asp	350	355	360
Phe Arg Trp Pro	Arg Thr Leu Ala Gly Ile Thr Ala Tyr Leu Gln	365	370	375
Cys Thr Arg Asn	Thr His Gly Ser Gly Ile Tyr Pro Gly Asn Pro			

<223> Synthetic construct

<400> 25

gaggactcac caatctgggtt cggc 24

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

aactggaaag gaaggctgtc tccc 24

<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 27

gtaaaggaga agaacatcac ggtacgggat accaggtgtg tttatcctaa 50

<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

gcgtggggat gtctaggagc tcgaagggtg tgctgggcct ctcggtgctg 50

ctgacggcgg ccacagtggc cggcgtacat gtgaagcagc agtgggacca 100

gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150

aaaaagaaaa cattcgtctt ttgggagaac agattatttt gactgagcaa 200

cttgaagcag aaagagagaa gatgttattg gcaaaaggat ctcaaaaatc 250

atgacttgaa tgtgaaatat ctgttgga gacaacacga gtttgtgtgt 300

gtgtgttgat ggagagtagc ttagtagtat cttcatcttt ttttttggtc 350

actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400

ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450

tttggaagag tctgtctggg tgatcctggt agaagcccca ttaggggtcac 500

tgtccagtgc ttagggttgt tactgagaag cactgccgag cttgtgagaa 550

ggaagggatg gatagtagca tccacctgag tagtctgatac agtcggcatg 600
 atgacgaagc cacgagaaca tcgacctcag aaggactgga ggaaggtgaa 650
 gtggagggag agacgctcct gatcgtcgaa tcc 683

<210> 29
 <211> 81
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> sig_peptide
 <222> 1-21
 <223> Signal peptide.

<400> 29
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 Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp
 20 25 30
 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
 35 40 45
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
 50 55 60
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
 65 70 75
 Lys Gly Ser Gln Lys Ser
 80

<210> 30
 <211> 2128
 <212> DNA
 <213> Homo sapiens

<400> 30
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 tacagcctgt tccaagtgtg gcttaatccg tctccaccac cagatctttc 100
 tccgtggatt cctctgctaa gaccgctgcc atgccagtga cggtaaccgc 150
 caccaccatc acaaccacca cgacgtcatc ttcgggcctg ggggtcccca 200
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 ctgctgcagc tgggtgtctac ctgcgtggcc ttctcgtcgtg tggctagcgt 300
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<210> 31
 <211> 322
 <212> PRT
 <213> Homo sapiens

<400> 31
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 35 40 45
 Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
 50 55 60
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
 65 70 75
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
 80 85 90
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
 95 100 105
 Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
 110 115 120
 Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
 125 130 135
 His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala
 140 145 150
 Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
 155 160 165
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
 170 175 180
 Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn
 185 190 195
 Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
 200 205 210

Ala	Ile	Cys	Phe	Ile	Leu	Ala	Ala	Ile	Ala	Ile	Leu	Leu	Asn	Leu	
				215					220					225	
Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu	
				230					235					240	
Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu	
				245					250					255	
Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln	
				260					265					270	
Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr	
				275					280					285	
Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr	
				290					295					300	
Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	Ala	
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<210> 32
 <211> 3680
 <212> DNA
 <213> Homo sapiens

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<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

Met	Phe	Leu	Ala	Thr	Leu	Ser	Phe	Leu	Leu	Pro	Phe	Ala	His	Pro
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Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
				20					25					30

Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45

His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60

Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75

Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90

Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
				95					100					105

Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
				110					115					120

Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg
				125					130					135

Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys
				140					145					150

Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp
				155					160					165

Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala
				170					175					180

Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly
				185					190					195

His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu
				200					205					210

Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser
				215					220					225

Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu
				230					235					240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
245 250 255

Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala
260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
275 280 285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
290 295 300

Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser
305 310 315

Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala
320 325 330

Glu Pro Glu Glu Gln
335

<210> 34
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct

<400> 34
tgtcctttgt cccagacttc tgtcc 25

<210> 35
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 35
ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcatgct 50

<210> 36
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 37
ggcgagccct aactatccag gag 23

<210> 38
<211> 39
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-39
<223> Synthetic construct.

<400> 38
ggagatcgct gcgctggcca ggtcctccct gcatggtat 39

<210> 39
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 39
ctgctgcaaa gcgagcctct tg 22

<210> 40
<211> 2084
<212> DNA
<213> Homo sapiens

<400> 40
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caacgttggtt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400
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<210> 41
<211> 334
<212> PRT
<213> Homo sapiens

<400> 41
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35 40 45
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
50 55 60
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
65 70 75
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
80 85 90
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
95 100 105
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
110 115 120
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
125 130 135
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
140 145 150
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
155 160 165
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
170 175 180
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
185 190 195

Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
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Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
				320					325					330

Arg Thr Ser Val

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
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aacttatgtg gttcgagaag acctagtgtc tgtggaggaa attcgtgatg 700
ttagtaacct tggcatcttt atttaccaac tttgcaataa cagaaaagtcc 750
ttccgccttc gtgcgagaga cctcttgctg ggtttcaaca aacgtgccat 800
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ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggttaata 900
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cctaacatcc tgacaataaa ttccatccgt tgtttttttt gtttgtttgt 1200
tttttctttt cctttaagta agctctttat tcatcttatg gtggagcaat 1250
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tatcagatct caacattgtt ggtttctttt gtttttcatt ttgtacaact 1350
ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400
ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450
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<210> 43
<211> 263
<212> PRT
<213> Homo sapiens

<400> 43
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Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg
20 25 30
Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
35 40 45
Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
gggaactgct atctgatgcc 20

<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
caggatctcc tcttcgagtc tgcagc 26

<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
cttctcgaac cacataagtt tgaggcag 28

<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
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 gtttcggcgg cagccccag cctcctcatc cttctgttgc tgctgctggg 200
 gtctgtgcct gctaccgacg cccgctctgt gccctgaag gccacgttcc 250
 tggaggatgt ggcgggtagt ggggaggccg agggctcgtc ggcctcctcc 300
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 ccggcagaag cagaaggcct cggcctatta cccatcgtec ttccccaaga 550
 agaagtacgt ggaccagagt gaccgggccg ggggccccg ggccttcagt 600
 gaggtccccg acagagcccc cgacagcagg cccgaggaag ccctggattc 650
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 ccccaccag ggctgcactg ggcggtgggg acggagccag gatggtggag 750
 ggcaggggcg cagaggaaga ggagaagggc agccaggagg gggaccagga 800
 agtccaggga catgggtcc cagtggagac accagaggcg caggaggagc 850
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 aatactgtc ttaattttcc tgaagggtgg cccctgtttc tagttggtcc 1450
 aggattaggg atgtggggta tagggcattt aaatcctctc aagcgctctc 1500

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 ggggctgggg aagggtttct gacgccagc ctggagcagg ggggccctgg 1700
 ccaccccctg ttgctcacac attgtctggc agcctgtgtc cacaatattc 1750
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 ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850
 gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900
 attccggcct gaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1950
 aaaaaaaaa aaaaaaaga 1969

<210> 50
 <211> 283
 <212> PRT
 <213> Homo sapiens

<400> 50
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 Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu
 20 25 30
 Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
 35 40 45
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
 50 55 60
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
 65 70 75
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
 80 85 90
 Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
 95 100 105
 Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
 110 115 120
 Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
 125 130 135
 Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
 140 145 150
 Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala
 155 160 165

Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr
				170					175					180
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp
				185					190					195
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys
				200					205					210
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro
				215					220					225
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu
				230					235					240
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly
				245					250					255
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro
				260					265					270
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val		
				275					280					

<210> 51
 <211> 1734
 <212> DNA
 <213> Homo sapiens

<400> 51
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 agacactctg gagagagagg gggctgggca gagatgaagt tccagggggc 200
 cctggcctgc ctctgtctgg ccctctgcct gggcagtggg gaggctggcc 250
 ccctgcagag cggagaggaa agcactggga caaatatttg ggaggccctt 300
 ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg 350
 caaagaggcc ggaggggag ctggctctaa agtcagttag gcccttggcc 400
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 ggcgagcag atgctttggg caacagggtc ggggaagcag cccatgtctt 500
 gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550
 acggagcaga tgctgtccgc ggctcctggc aggggggtgcc tggccacagt 600
 ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaaggtgg 650
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tccaaggata ccccggaac tcagcaggca gctttggaat gaatcctcag 750
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 ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtg 950
 cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000
 gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc 1050
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 tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52
 <211> 440
 <212> PRT
 <213> Homo sapiens

<400> 52
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 Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser
 20 25 30
 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
 35 40 45
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

50					55					60				
Gly	Ala	Ala	Gly	Ser	Lys	Val	Ser	Glu	Ala	Leu	Gly	Gln	Gly	Thr
				65					70					75
Arg	Glu	Ala	Val	Gly	Thr	Gly	Val	Arg	Gln	Val	Pro	Gly	Phe	Gly
				80					85					90
Ala	Ala	Asp	Ala	Leu	Gly	Asn	Arg	Val	Gly	Glu	Ala	Ala	His	Ala
				95					100					105
Leu	Gly	Asn	Thr	Gly	His	Glu	Ile	Gly	Arg	Gln	Ala	Glu	Asp	Val
				110					115					120
Ile	Arg	His	Gly	Ala	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val
				125					130					135
Pro	Gly	His	Ser	Gly	Ala	Trp	Glu	Thr	Ser	Gly	Gly	His	Gly	Ile
				140					145					150
Phe	Gly	Ser	Gln	Gly	Gly	Leu	Gly	Gly	Gln	Gly	Gln	Gly	Asn	Pro
				155					160					165
Gly	Gly	Leu	Gly	Thr	Pro	Trp	Val	His	Gly	Tyr	Pro	Gly	Asn	Ser
				170					175					180
Ala	Gly	Ser	Phe	Gly	Met	Asn	Pro	Gln	Gly	Ala	Pro	Trp	Gly	Gln
				185					190					195
Gly	Gly	Asn	Gly	Gly	Pro	Pro	Asn	Phe	Gly	Thr	Asn	Thr	Gln	Gly
				200					205					210
Ala	Val	Ala	Gln	Pro	Gly	Tyr	Gly	Ser	Val	Arg	Ala	Ser	Asn	Gln
				215					220					225
Asn	Glu	Gly	Cys	Thr	Asn	Pro	Pro	Pro	Ser	Gly	Ser	Gly	Gly	Gly
				230					235					240
Ser	Ser	Asn	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gln	Ser	Gly	Ser	Ser
				245					250					255
Gly	Ser	Gly	Ser	Asn	Gly	Asp	Asn	Asn	Asn	Gly	Ser	Ser	Ser	Gly
				260					265					270
Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Gly	Ser
				275					280					285
Ser	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser	Gly	Asn	Ser	Gly	Gly	Ser
				290					295					300
Arg	Gly	Asp	Ser	Gly	Ser	Glu	Ser	Ser	Trp	Gly	Ser	Ser	Thr	Gly
				305					310					315
Ser	Ser	Ser	Gly	Asn	His	Gly	Gly	Ser	Gly	Gly	Gly	Asn	Gly	His
				320					325					330
Lys	Pro	Gly	Cys	Glu	Lys	Pro	Gly	Asn	Glu	Ala	Arg	Gly	Ser	Gly
				335					340					345

Glu	Ser	Gly	Ile	Gln	Gly	Phe	Arg	Gly	Gln	Gly	Val	Ser	Ser	Asn
				350					355					360
Met	Arg	Glu	Ile	Ser	Lys	Glu	Gly	Asn	Arg	Leu	Leu	Gly	Gly	Ser
				365					370					375
Gly	Asp	Asn	Tyr	Arg	Gly	Gln	Gly	Ser	Ser	Trp	Gly	Ser	Gly	Gly
				380					385					390
Gly	Asp	Ala	Val	Gly	Gly	Val	Asn	Thr	Val	Asn	Ser	Glu	Thr	Ser
				395					400					405
Pro	Gly	Met	Phe	Asn	Phe	Asp	Thr	Phe	Trp	Lys	Asn	Phe	Lys	Ser
				410					415					420
Lys	Leu	Gly	Phe	Ile	Asn	Trp	Asp	Ala	Ile	Asn	Lys	Asp	Gln	Arg
				425					430					435
Ser	Ser	Arg	Ile	Pro										
				440										

<210> 53
 <211> 3580
 <212> DNA
 <213> Homo sapiens

<400> 53
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 ctttgctgac catgttggtc ccttgctgga atattaccgg gacatcttca 150
 ctctcctgct ggcctgcac cggagcttgg tgttgctgca ggagagtgg 200
 gggaagatgt gtttcctgaa caagctgctg ctacttgctg tcttgggctg 250
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 gacaatgcgc ctgtggtgga ccagcagctg ctctacacct gctgccccta 400
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 ggtgacacag ggagaggaag ggggagacct agcccagctg ttggagatct 750
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ttattagctg ggcattggtg tgtgtgcctg taatcccagc tactcaggag 2300
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<210> 54
 <211> 280
 <212> PRT
 <213> Homo sapiens

<400> 54

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				20					25					30
Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu
				35					40					45
His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
				50					55					60
Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
				65					70					75
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
				80					85					90
Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
				95					100					105
Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
				110					115					120
Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
				125					130					135
Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val
				140					145					150
Ala	Asp	Leu	Val	Arg	Gln	Ala	Glu	Ser	Leu	Leu	Gln	Glu	Gln	Leu
				155					160					165
Val	Thr	Gln	Gly	Glu	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu
				170					175					180
Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala
				185					190					195
Leu	Gly	Arg	Glu	Phe	Cys	Gln	Arg	Lys	Ser	Pro	Gly	Ala	Val	Arg
				200					205					210
Ala	Leu	Leu	Pro	Glu	Glu	Thr	Pro	Ala	Ala	Val	Leu	Ser	Ser	Ala
				215					220					225
Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp
				230					235					240
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
				245					250					255
Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala
				260					265					270
Arg	Gly	Glu	Arg	Arg	Gly	Cys	Ser	Arg	Ala					
				275					280					

<210> 55
<211> 2401
<212> DNA
<213> Homo sapiens

<400> 55
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ccttgaggtg tgaaccaca tccctgcccc cagggccacc tgcaggacgc 150
cgacacctac ccctcagcag acgccggaga gaaatgagta gcaacaaaga 200
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<210> 56

<211> 299

<212> PRT

<213> Homo sapiens

<400> 56

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Phe Ala Leu Ile Thr Ile Leu Ile Leu Tyr Ser Ser Asn Ser Ala
      20             25             30

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Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro	
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Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg	
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Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly	
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Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro	
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Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly	
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 <212> DNA
 <213> Homo sapiens

<400> 57

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<210> 58
 <211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

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Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	
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Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	
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Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	
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Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	
				95					100					105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	
				110					115					120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	
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His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	
				140					145					150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	
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Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	
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Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	
				185					190					195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	
				200					205					210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	
				215					220					225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	
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Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	
				245					250					255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	
				260					265					270	

Val Thr Gly Tyr	Asn Lys Thr Arg Phe	Leu Leu Ser Asn Leu Leu	275	280	285
Ile Asp Thr Thr	Ser Glu Glu Asp Ser	Gly Thr Tyr Arg Cys Met	290	295	300
Ala Asp Asn Gly	Val Gly Gln Pro Gly	Ala Ala Val Ile Leu Tyr	305	310	315
Asn Val Gln Val	Phe Glu Pro Pro Glu	Val Thr Met Glu Leu Ser	320	325	330
Gln Leu Val Ile	Pro Trp Gly Gln Ser	Ala Lys Leu Thr Cys Glu	335	340	345
Val Arg Gly Asn	Pro Pro Pro Ser Val	Leu Trp Leu Arg Asn Ala	350	355	360
Val Pro Leu Ile	Ser Ser Gln Arg Leu	Arg Leu Ser Arg Arg Ala	365	370	375
Leu Arg Val Leu	Ser Met Gly Pro Glu	Asp Glu Gly Val Tyr Gln	380	385	390
Cys Met Ala Glu	Asn Glu Val Gly Ser	Ala His Ala Val Val Gln	395	400	405
Leu Arg Thr Ser	Arg Pro Ser Ile Thr	Pro Arg Leu Trp Gln Asp	410	415	420
Ala Glu Leu Ala	Thr Gly Thr Pro Pro	Val Ser Pro Ser Lys Leu	425	430	435
Gly Asn Pro Glu	Gln Met Leu Arg Gly	Gln Pro Ala Leu Pro Arg	440	445	450
Pro Pro Thr Ser	Val Gly Pro Ala Ser	Pro Lys Cys Pro Gly Glu	455	460	465
Lys Gly Gln Gly	Ala Pro Ala Glu Ala	Pro Ile Ile Leu Ser Ser	470	475	480
Pro Arg Thr Ser	Lys Thr Asp Ser Tyr	Glu Leu Val Trp Arg Pro	485	490	495
Arg His Glu Gly	Ser Gly Arg Ala Pro	Ile Leu Tyr Tyr Val Val	500	505	510
Lys His Arg Lys	Gln Val Thr Asn Ser	Ser Asp Asp Trp Thr Ile	515	520	525
Ser Gly Ile Pro	Ala Asn Gln His Arg	Leu Thr Leu Thr Arg Leu	530	535	540
Asp Pro Gly Ser	Leu Tyr Glu Val Glu	Met Ala Ala Tyr Asn Cys	545	550	555
Ala Gly Glu Gly	Gln Thr Ala Met Val	Thr Phe Arg Thr Gly Arg			

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Arg Pro Lys Pro	Glu Ile Met Ala Ser	Lys Glu Gln Gln Ile Gln			
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Arg Asp Asp Pro	Gly Ala Ser Pro Gln	Ser Ser Ser Gln Pro Asp			
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His Gly Arg Leu	Ser Pro Pro Glu Ala	Pro Asp Arg Pro Thr Ile			
	605	610			615
Ser Thr Ala Ser	Glu Thr Ser Val Tyr	Val Thr Trp Ile Pro Arg			
	620	625			630
Gly Asn Gly Gly	Phe Pro Ile Gln Ser	Phe Arg Val Glu Tyr Lys			
	635	640			645
Lys Leu Lys Lys	Val Gly Asp Trp Ile	Leu Ala Thr Ser Ala Ile			
	650	655			660
Pro Pro Ser Arg	Leu Ser Val Glu Ile	Thr Gly Leu Glu Lys Gly			
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Thr Ser Tyr Lys	Phe Arg Val Arg Ala	Leu Asn Met Leu Gly Glu			
	680	685			690
Ser Glu Pro Ser	Ala Pro Ser Arg Pro	Tyr Val Val Ser Gly Tyr			
	695	700			705
Ser Gly Arg Val	Tyr Glu Arg Pro Val	Ala Gly Pro Tyr Ile Thr			
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Phe Thr Asp Ala	Val Asn Glu Thr Thr	Ile Met Leu Lys Trp Met			
	725	730			735
Tyr Ile Pro Ala	Ser Asn Asn Asn Thr	Pro Ile His Gly Phe Tyr			
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Ile Tyr Tyr Arg	Pro Thr Asp Ser Asp	Asn Asp Ser Asp Tyr Lys			
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Lys Asp Met Val	Glu Gly Asp Lys Tyr	Trp His Ser Ile Ser His			
	770	775			780
Leu Gln Pro Glu	Thr Ser Tyr Asp Ile	Lys Met Gln Cys Phe Asn			
	785	790			795
Glu Gly Gly Glu	Ser Glu Phe Ser Asn	Val Met Ile Cys Glu Thr			
	800	805			810
Lys Ala Arg Lys	Ser Ser Gly Gln Pro	Gly Arg Leu Pro Pro Pro			
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Thr Leu Ala Pro	Pro Gln Pro Pro Leu	Pro Glu Thr Ile Glu Arg			
	830	835			840
Pro Val Gly Thr	Gly Ala Met Val Ala	Arg Ser Ser Asp Leu Pro			
	845	850			855

Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	860	865	870
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Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	890	895	900
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His	905	910	915
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala	920	925	930
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Pro	Lys	Ser	Ser	Pro	Asp	Glu	Gly	Ser	Phe	Leu	Tyr	Thr	Leu	Pro	995	1000	1005
Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Cys	1010	1015	1020
Gln	Arg	Gln	Glu	Gln	Pro	Ala	Ala	Val	Gly	Gln	Ser	Gly	Val	Arg	1025	1030	1035
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Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu	1055	1060	1065
Glu	Val	Asp	Ser	Pro	Asp	Ser	Cys	Gln	Val	Ser	Gly	Gly	Asp	Trp	1070	1075	1080
Cys	Pro	Gln	His	Pro	Val	Gly	Ala	Tyr	Val	Gly	Gln	Glu	Pro	Gly	1085	1090	1095
Met	Gln	Leu	Ser	Pro	Gly	Pro	Leu	Val	Arg	Val	Ser	Phe	Glu	Thr	1100	1105	1110
Pro	Pro	Leu	Thr	Ile											1115		

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<211> 25

<212> DNA

<213> Artificial

<220>
<221> Artificial sequence
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<223> Synthetic construct.

<400> 59
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<210> 60
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 60
gcacacgtag cctgtcgctg gaggc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-42
<223> Synthetic construct.

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<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

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<222> 678
<223> unknown base

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cacttacott cacctgcagt acaccatggg cagagagttc caccaagttc 800
agacaccaca tgtacaccaa cgtcagcggc ttgacaagct ttggtgagaa 850
agtagtagag gagttgaacc gcctgggcat gatgatagat ttgtcctatg 900
catcggacac cttgataaga agggctcctg aagtgtctca ggctcctgtg 950
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cgggattggg ggaaattatg acgggactgg ccggttcctc caggggctgg 1200
aggatgtgtc cacataccca gtcctgatag aggagttgct gagtcgtasc 1250
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tgctgacaca gtcgggtccc gcagagggtca ctgtggcaaa gcctcacaaa 1600
gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650
cacatggaaa a 1661

<210> 63
<211> 487
<212> PRT
<213> Homo sapiens

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg	1	5	10	15
Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	20	25	30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	35	40	45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	50	55	60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	65	70	75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	80	85	90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	95	100	105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	110	115	120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	125	130	135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	140	145	150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	155	160	165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	170	175	180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	185	190	195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	200	205	210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	215	220	225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	230	235	240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	245	250	255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala				

260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu	Glu Val Ser Gln Ala Pro	
275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg	Ala Val Cys Asp Asn Leu	
290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln	Leu Leu Lys Asn Gly Gly	
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly	Val Leu Gln Cys Asn Leu	
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp	His Phe Asp His Ile Arg	
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly	Ile Gly Gly Asn Tyr Asp	
350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu	Glu Asp Val Ser Thr Tyr	
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser	Arg Xaa Trp Ser Glu Glu	
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn	Leu Leu Arg Val Phe Arg	
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser	Arg Ala Gln Ser Pro Val	
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu	Ser Thr Ser Cys His Ser	
425	430	435
His Leu Val Pro Gln Asn Gly His Gln	Ala Thr His Leu Glu Val	
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro	Trp Arg Ser Ser Asn Ala	
455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val	Ala Ala Ala Thr Ile Pro	
470	475	480
Thr Phe Thr Gln Trp Leu Cys		
485		

<210> 64

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 65

gtcacacaca gctctggcag ctgag 25

<210> 66

<211> 47

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-47

<223> Synthetic construct.

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50

aacaccacaca gatccctcta tgactgcaat gtgagggtgc cggttttgc 100

ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150

cggtgtgttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200

tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250

tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300

gcccattgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350

agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400

atctacctgt ccgtggtggg tgcctgttg ctctacatgg ccttctgat 450

gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500

acaatgagga ggagaatgag gatgctcgt ctatggcagc agctgctgca 550

tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaagggtgc 600

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 ccaacacccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750
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 cgctgtcccc tgtgcacttc tcgcactggg gcatggagtg cccatgcata 1300
 ctctgtctgcc ggtcccctca cctgcacttg aggggtcttg gcagtccttc 1350
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 gactcgaggc tgagcgtgga tctgaacacc acagcccctg tacttggggt 1450
 gcctcttgtc cctgaacttc gttgtaccag tgcattggaga gaaaattttg 1500
 tcctcttgtc ttagagttgt gtgtaaatca aggaagccat cattaaattg 1550
 ttttatttct ctca 1564

<210> 68
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
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 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
 20 25 30
 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
 35 40 45
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
 50 55 60

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu
				65					70					75
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val
				80					85					90
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr
				95					100					105
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp
				110					115					120
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala
				125					130					135
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala
				140					145					150
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys
				155					160					165
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys
				170					175					180

Met Leu Ser

<210> 69
 <211> 3170
 <212> DNA
 <213> Homo sapiens

<400> 69
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 agttcatagg gtcttgggtc cccgaaccag gaagggttga gggaacacaa 100
 tctgcaagcc cccgcgaccc aagtgagggg ccccggtgtg gggtcctccc 150
 tccctttgca tccccacccc tccgggcttt gcgtcttcct ggggaccccc 200
 tcgccgggag atggccgcgt tgatgcggag caaggattcg tcctgctgcc 250
 tgctcctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300
 tcgcggggcca aactcaactc catcaagtcc tctctgggcg gggagacgcc 350
 tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400
 gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 450
 gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500
 atcggcctgc atggtgtgtc ggagaaaaaa gaagcgtgc caccgagatg 550
 gcatgtgctg cccagtagcc cgctgcaata atggcatctg tatcccagtt 600
 actgaaagca tcttaacccc tcacatcccg gctctggatg gtactcggca 650

cagagatoga aaccacggtc attactcaaa ccatgacttg ggatggcaga 700
atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750
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 aaaaaaaaaa aaaaaaaaaa 3170

<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

Met	Ala	Ala	Leu	Met	Arg	Ser	Lys	Asp	Ser	Ser	Cys	Cys	Leu	Leu
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Leu	Leu	Ala	Ala	Val	Leu	Met	Val	Glu	Ser	Ser	Gln	Ile	Gly	Ser
				20					25					30

Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
				35					40					45

Thr	Pro	Gly	Gln	Ala	Ala	Asn	Arg	Ser	Ala	Gly	Met	Tyr	Gln	Gly	
				50					55					60	
Leu	Ala	Phe	Gly	Gly	Ser	Lys	Lys	Gly	Lys	Asn	Leu	Gly	Gln	Ala	
				65					70					75	
Tyr	Pro	Cys	Ser	Ser	Asp	Lys	Glu	Cys	Glu	Val	Gly	Arg	Tyr	Cys	
				80					85					90	
His	Ser	Pro	His	Gln	Gly	Ser	Ser	Ala	Cys	Met	Val	Cys	Arg	Arg	
				95					100					105	
Lys	Lys	Lys	Arg	Cys	His	Arg	Asp	Gly	Met	Cys	Cys	Pro	Ser	Thr	
				110					115					120	
Arg	Cys	Asn	Asn	Gly	Ile	Cys	Ile	Pro	Val	Thr	Glu	Ser	Ile	Leu	
				125					130					135	
Thr	Pro	His	Ile	Pro	Ala	Leu	Asp	Gly	Thr	Arg	His	Arg	Asp	Arg	
				140					145					150	
Asn	His	Gly	His	Tyr	Ser	Asn	His	Asp	Leu	Gly	Trp	Gln	Asn	Leu	
				155					160					165	
Gly	Arg	Pro	His	Thr	Lys	Met	Ser	His	Ile	Lys	Gly	His	Glu	Gly	
				170					175					180	
Asp	Pro	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ile	Glu	Gly	Phe	Cys	Cys	
				185					190					195	
Ala	Arg	His	Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	His	Gln	
				200					205					210	
Gly	Glu	Val	Cys	Thr	Lys	Gln	Arg	Lys	Lys	Gly	Ser	His	Gly	Leu	
				215					220					225	
Glu	Ile	Phe	Gln	Arg	Cys	Asp	Cys	Ala	Lys	Gly	Leu	Ser	Cys	Lys	
				230					235					240	
Val	Trp	Lys	Asp	Ala	Thr	Tyr	Ser	Ser	Lys	Ala	Arg	Leu	His	Val	
				245					250					255	

Cys Gln Lys Ile

<210> 71
 <211> 1809
 <212> DNA
 <213> Homo sapiens

<400> 71
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 acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150
 cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

tagtcagttt tcattgcata gtaatatatt catgtagtat tttctaagtt 250
atatatttagt aattcatatg ttttagatta taggttttaa catacttgtg 300
aaaataacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350
ggatttgttc ttttatcccc cttttaaagt catccgtcct tggctcagga 400
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gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550
ctcaagcccc caacatccca gtcctcagtc ctcagtcatc ttgacttcaa 600
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tttaaagatg cttgggccag gcgggggtgc tgatgcccat aatcccagtg 1600
ctttgggggg ccaaggcag cagattgccc aagctcagga gtttgagacc 1650

accctgggca acatggtgaa actctgtctc tactaaaata cgaaaaacta 1700
gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttgggaggct 1750
gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800
ctgaaaaga 1809

<210> 72
<211> 363
<212> PRT
<213> Homo sapiens

<400> 72
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1 5 10 15
Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly
20 25 30
Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
35 40 45
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
50 55 60
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
65 70 75
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
80 85 90
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
95 100 105
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
110 115 120
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
125 130 135
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
140 145 150
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
155 160 165
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
170 175 180
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
185 190 195
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
200 205 210
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
215 220 225

Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser
				275					280					285
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln
				290					295					300
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn
				305					310					315
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr
				320					325					330
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg
				335					340					345
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp
				350					355					360

Leu Ile Arg

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 73
 aattcatggc aaatatttcc cttccc 26

<210> 74
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 74
 tggtaaactg gcccaaactc gg 22

<210> 75
 <211> 50

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
ttaaagtcac cgcgccttgg ctcaggattt ggagagcttg caccaccaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
gccgagtggg acaaagcctg gggctgggcg ggggccatgg cgctgccatc 50
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tgactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150
caccatcact actgccacct ctacgagagc ctggccgtcc gcctggaggt 200
caccgacggc cccccggcca cccccgcta ctgggacggc gagaaggagg 250
tgctggcggg ggcgcgcggc gcacccgcgc ttctgacctg cgtgaaccgc 300
gggcacgtgt ggaccgaccg gcacgtggag gaggtcaac aggtggtgca 350
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caataaagtc cccatctgat ttttaaaaaa aaaaaaaaa 1989

<210> 77
<211> 341
<212> PRT
<213> Homo sapiens

<400> 77
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Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp
20 25 30
Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
35 40 45
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
50 55 60
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
65 70 75

Ala Arg Gly Ala	Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His	80	85	90
Val Trp Thr Asp	Arg His Val Glu Glu Ala Gln Gln Val Val His	95	100	105
Trp Asp Arg Gln	Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg	110	115	120
Leu Leu Asp Leu	Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro	125	130	135
Leu Phe Leu Arg	Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu	140	145	150
Arg Gly Asp Phe	Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp	155	160	165
Glu Gly Thr Tyr	Ser Cys His Leu His His His Tyr Cys Gly Leu	170	175	180
His Glu Arg Arg	Val Phe His Leu Thr Val Ala Glu Pro His Ala	185	190	195
Glu Pro Pro Pro	Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser	200	205	210
Gly Ala Pro Gly	Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val	215	220	225
Ile Asn Val Ile	Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln	230	235	240
Leu Gly Tyr Val	Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu	245	250	255
Val Thr Val Leu	Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu	260	265	270
Tyr Ser Asp Gln	Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn	275	280	285
Leu Ala Glu Phe	Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg	290	295	300
Ser Glu Asp Ile	Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu	305	310	315
Arg Ala Glu Leu	Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp	320	325	330
Leu Asp Lys Gly	Phe Arg Lys Glu Asn Cys Lys	335	340	

<210> 78
 <211> 2243
 <212> DNA
 <213> Homo sapiens

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taaagtttca cttggggaca gagagcagag cacactcggg cctcatccct 1600
cccaagatgc cagttagcca cgtccatgcc cattccgtgc aaggcagata 1650
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gccattggtt caagggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79
<211> 475
<212> PRT
<213> Homo sapiens

<400> 79
Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser
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Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala
20 25 30
Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
35 40 45
Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
50 55 60
Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
65 70 75
Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
80 85 90
Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
95 100 105

Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135
Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr	140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	155	160	165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	365	370	375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	380	385	390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys			

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Thr Val Val Phe Gln Ser Asp Val Tyr	Pro Ala Leu Leu Ser Ser		
410	415	420	
Leu Leu Gly Leu Ser Asn Gly Tyr Leu	Ser Thr Leu Ala Leu Leu		
425	430	435	
Tyr Gly Pro Lys Ile Val Pro Arg Glu	Leu Ala Glu Ala Thr Gly		
440	445	450	
Val Val Met Ser Phe Tyr Val Cys Leu	Gly Leu Thr Leu Gly Ser		
455	460	465	
Ala Cys Ser Thr Leu Leu Val His Leu	Ile		
470	475		

<210> 80
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 80
ttttgcggtc accattgtct gc 22

<210> 81
<211> 23
<212> DNA
<213> Homo sapiens

<220>
<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 81
cgtaggtgac acagaagccc agg 23

<210> 82
<211> 49
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-49
<223> Synthetic construct.

<400> 82
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<210> 83
<211> 1844

<212> DNA
<213> Homo sapiens

<400> 83

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cacaagctct gccagggcct ggggctcaac ctgaccaagt tcaccagta 500
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84
 <211> 567
 <212> PRT
 <213> Homo sapiens

<400> 84
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 20 25 30
 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu
 35 40 45
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
 50 55 60
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
 65 70 75
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
 80 85 90
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
 95 100 105
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
 110 115 120
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
 125 130 135
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
 140 145 150
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
 155 160 165

455 460 465

Lys	Asp	Asp	Trp	Thr	Val	Pro	Tyr	Gly	Arg	Ile	Tyr	Phe	Ala	Gly	455	460	465
				470					475					480			
Glu	His	Thr	Ala	Tyr	Pro	His	Gly	Trp	Val	Glu	Thr	Ala	Val	Lys			
				485					490					495			
Ser	Ala	Leu	Arg	Ala	Ala	Ile	Lys	Ile	Asn	Ser	Arg	Lys	Gly	Pro			
				500					505					510			
Ala	Ser	Asp	Thr	Ala	Ser	Pro	Glu	Gly	His	Ala	Ser	Asp	Met	Glu			
				515					520					525			
Gly	Gln	Gly	His	Val	His	Gly	Val	Ala	Ser	Ser	Pro	Ser	His	Asp			
				530					535					540			
Leu	Ala	Lys	Glu	Glu	Gly	Ser	His	Pro	Pro	Val	Gln	Gly	Gln	Leu			
				545					550					555			
Ser	Leu	Gln	Asn	Thr	Thr	His	Thr	Arg	Thr	Ser	His						
				560					565								

<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

<400> 85
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gcaccagaga agatagaaaa tatctacaac aggagtcaac cagtgttaca 1950
aatttttgta cacggggaga gcttacggtc atccttagta ggagtgggtg 2000
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 ctatcactca tgtcaatcat atctatgaga caaatgtctc cgatgctctt 2850
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 atttcctaaa ctctctagtt agatatctga cttggggagta ttaaaaattg 2950
 ggtctatgac atactgtcca aaaggaatgc tgttcttaaa gcattattta 3000
 cagtaggaac tggggagtaa atctgttccc tacagtttgc tgctgagctg 3050
 gaagctgtgg ggggaaggagt tgacaggtgg gccagtgaa cttttccagt 3100
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 aactgatctc cccaccctt ggattagagt tcctgctcta ccttaccac 3250
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<210> 86
 <211> 739
 <212> PRT
 <213> Homo sapiens

<400> 86
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 Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro
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Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser	
				35					40					45	
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile	
				50					55					60	
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys	
				65					70					75	
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg	
				80					85					90	
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val	
				95					100					105	
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn	
				110					115					120	
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu	
				125					130					135	
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu	
				140					145					150	
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys	
				155					160					165	
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His	
				170					175					180	
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala	
				185					190					195	
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr	
				200					205					210	
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu	
				215					220					225	
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile	
				230					235					240	
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu	
				245					250					255	
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro	
				260					265					270	
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu	
				275					280					285	
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe	
				290					295					300	
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys	
				305					310					315	
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr	

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His Gln Asn Ile	Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys	Val		
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Glu His Ala Tyr	Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser	Tyr		
	350		355		360
Leu Pro Leu Ala	His Met Phe Glu Arg	Ile Val Gln Ala Val	Val		
	365		370		375
Tyr Ser Cys Gly	Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile	Arg		
	380		385		390
Leu Leu Ala Asp	Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe	Pro		
	395		400		405
Ala Val Pro Arg	Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln	Asn		
	410		415		420
Glu Ala Lys Thr	Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala	Val		
	425		430		435
Ser Ser Lys Phe	Lys Glu Leu Gln Lys	Gly Ile Ile Arg His	Asp		
	440		445		450
Ser Phe Trp Asp	Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser	Leu		
	455		460		465
Gly Gly Arg Val	Arg Val Ile Val Thr	Gly Ala Ala Pro Met	Ser		
	470		475		480
Thr Ser Val Met	Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln	Val		
	485		490		495
Tyr Glu Ala Tyr	Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr	Phe		
	500		505		510
Thr Leu Pro Gly	Asp Trp Thr Ser Gly	His Val Gly Val Pro	Leu		
	515		520		525
Ala Cys Asn Tyr	Val Lys Leu Glu Asp	Val Ala Asp Met Asn	Tyr		
	530		535		540
Phe Thr Val Asn	Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr	Asn		
	545		550		555
Val Phe Lys Gly	Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu	Ala		
	560		565		570
Leu Asp Ser Asp	Gly Trp Leu His Thr	Gly Asp Ile Gly Arg	Trp		
	575		580		585
Leu Pro Asn Gly	Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn	Ile		
	590		595		600
Phe Lys Leu Ala	Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile	Glu		
	605		610		615

Asn	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
				620					625					630
Gly	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
				635					640					645
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
				650					655					660
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
				665					670					675
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
				680					685					690
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
				695					700					705
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
				710					715					720
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
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His Ile Gln Asp

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 <211> 2725
 <212> DNA
 <213> Homo sapiens

<400> 87
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 cccctcatca agccctttgg ggctcggaag aagcggagct ggtaccttac 200
 ctggaagtat aaactgacaa accagcgggc cctgcggaga ttctgtcaga 250
 cagggggccgt gcttttcctg ctggtgactg tcattgtcaa tatcaagttg 300
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<210> 88
 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 88
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 35 40 45
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
 50 55 60
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
 65 70 75
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
 80 85 90
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
 95 100 105
 Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
 110 115 120
 Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
 125 130 135

Leu	Asn	Gln	Ala	Thr	Gly	His	Val	Met	Ala	Lys	Arg	Val	Phe	Asp	
				140					145					150	
Thr	Tyr	Ser	Pro	His	Glu	Asp	Glu	Ala	Met	Val	Leu	Phe	Leu	Asn	
				155					160					165	
Met	Val	Ala	Pro	Gly	Arg	Val	Leu	Ile	Cys	Thr	Val	Lys	Asp	Glu	
				170					175					180	
Gly	Ser	Phe	His	Leu	Lys	Asp	Thr	Ala	Lys	Ala	Leu	Leu	Arg	Ser	
				185					190					195	
Leu	Gly	Ser	Gln	Ala	Gly	Pro	Ala	Leu	Gly	Trp	Arg	Asp	Thr	Trp	
				200					205					210	
Ala	Phe	Val	Gly	Arg	Lys	Gly	Gly	Pro	Val	Phe	Gly	Glu	Lys	His	
				215					220					225	
Ser	Lys	Ser	Pro	Ala	Leu	Ser	Ser	Trp	Gly	Asp	Pro	Val	Leu	Leu	
				230					235					240	
Lys	Thr	Asp	Val	Pro	Leu	Ser	Ser	Ala	Glu	Glu	Ala	Glu	Cys	His	
				245					250					255	
Trp	Ala	Asp	Thr	Glu	Leu	Asn	Arg	Arg	Arg	Arg	Arg	Phe	Cys	Ser	
				260					265					270	
Lys	Val	Glu	Gly	Tyr	Gly	Ser	Val	Cys	Ser	Cys	Lys	Asp	Pro	Thr	
				275					280					285	
Pro	Ile	Glu	Phe	Ser	Pro	Asp	Pro	Leu	Pro	Asp	Asn	Lys	Val	Leu	
				290					295					300	
Asn	Val	Pro	Val	Ala	Val	Ile	Ala	Gly	Asn	Arg	Pro	Asn	Tyr	Leu	
				305					310					315	
Tyr	Arg	Met	Leu	Arg	Ser	Leu	Leu	Ser	Ala	Gln	Gly	Val	Ser	Pro	
				320					325					330	
Gln	Met	Ile	Thr	Val	Phe	Ile	Asp	Gly	Tyr	Tyr	Glu	Glu	Pro	Met	
				335					340					345	
Asp	Val	Val	Ala	Leu	Phe	Gly	Leu	Arg	Gly	Ile	Gln	His	Thr	Pro	
				350					355					360	
Ile	Ser	Ile	Lys	Asn	Ala	Arg	Val	Ser	Gln	His	Tyr	Lys	Ala	Ser	
				365					370					375	
Leu	Thr	Ala	Thr	Phe	Asn	Leu	Phe	Pro	Glu	Ala	Lys	Phe	Ala	Val	
				380					385					390	
Val	Leu	Glu	Glu	Asp	Leu	Asp	Ile	Ala	Val	Asp	Phe	Phe	Ser	Phe	
				395					400					405	
Leu	Ser	Gln	Ser	Ile	His	Leu	Leu	Glu	Glu	Asp	Asp	Ser	Leu	Tyr	
				410					415					420	
Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu	

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Asp	Pro	Ala	Leu	Leu	Tyr	Arg	Val	Glu	Thr	Met	Pro	Gly	Leu	Gly
			440						445					450
Trp	Val	Leu	Arg	Arg	Ser	Leu	Tyr	Lys	Glu	Glu	Leu	Glu	Pro	Lys
			455						460					465
Trp	Pro	Thr	Pro	Glu	Lys	Leu	Trp	Asp	Trp	Asp	Met	Trp	Met	Arg
			470						475					480
Met	Pro	Glu	Gln	Arg	Arg	Gly	Arg	Glu	Cys	Ile	Ile	Pro	Asp	Val
			485						490					495
Ser	Arg	Ser	Tyr	His	Phe	Gly	Ile	Val	Gly	Leu	Asn	Met	Asn	Gly
			500						505					510
Tyr	Phe	His	Glu	Ala	Tyr	Phe	Lys	Lys	His	Lys	Phe	Asn	Thr	Val
			515						520					525
Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser	Leu	Lys	Lys	Glu	Ala
			530						535					540
Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu	Ala	Glu	Val	Leu
			545						550					555
Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu	Pro	Asp	Thr
			560						565					570
Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys	Asp	Asp
			575						580					585
Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile	Trp
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Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe
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Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro
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Tyr	Ser	Val	Lys	Lys	Pro	Pro	Ser	Val	Thr	Pro	Ile	Phe	Leu	Glu
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 <212> DNA
 <213> Artificial

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 <223> Synthetic construct.

 <400> 89

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<210> 90
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<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 90
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<210> 91
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<212> DNA
<213> Artificial

<220>
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<222> 1-24
<223> Synthetic construct.

<400> 91
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<210> 92
<211> 26
<212> DNA
<213> Artificial

<220>
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<223> Synthetic construct.

<400> 92
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<210> 93
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 93
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<210> 94
<211> 3037
<212> DNA
<213> Homo sapiens

<400> 94

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 tcagcagctg tggaataaaa gcttgtgagc cctctgctgg ccacagtgag 2800
 gaaagtagca caaataggat acagttgtat gtagtcattg gcaacaattg 2850
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<210> 95
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 95

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Val	Gly	Cys	Tyr	Val	Ala	Gly	Ile	Ile	Pro	Leu	Ala	Val	Asn	Phe	
				20					25					30	
Ser	Glu	Glu	Arg	Leu	Lys	Leu	Val	Thr	Val	Leu	Gly	Ala	Gly	Leu	
				35					40					45	
Leu	Cys	Gly	Thr	Ala	Leu	Ala	Val	Ile	Val	Pro	Glu	Gly	Val	His	
				50					55					60	
Ala	Leu	Tyr	Glu	Asp	Ile	Leu	Glu	Gly	Lys	His	His	Gln	Ala	Ser	
				65					70					75	
Glu	Thr	His	Asn	Val	Ile	Ala	Ser	Asp	Lys	Ala	Ala	Glu	Lys	Ser	
				80					85					90	
Val	Val	His	Glu	His	Glu	His	Ser	His	Asp	His	Thr	Gln	Leu	His	
				95					100					105	
Ala	Tyr	Ile	Gly	Val	Ser	Leu	Val	Leu	Gly	Phe	Val	Phe	Met	Leu	
				110					115					120	
Leu	Val	Asp	Gln	Ile	Gly	Asn	Ser	His	Val	His	Ser	Thr	Asp	Asp	
				125					130					135	
Pro	Glu	Ala	Ala	Arg	Ser	Ser	Asn	Ser	Lys	Ile	Thr	Thr	Thr	Leu	
				140					145					150	
Gly	Leu	Val	Val	His	Ala	Ala	Ala	Asp	Gly	Val	Ala	Leu	Gly	Ala	
				155					160					165	
Ala	Ala	Ser	Thr	Ser	Gln	Thr	Ser	Val	Gln	Leu	Ile	Val	Phe	Val	
				170					175					180	
Ala	Ile	Met	Leu	His	Lys	Ala	Pro	Ala	Ala	Phe	Gly	Leu	Val	Ser	
				185					190					195	
Phe	Leu	Met	His	Ala	Gly	Leu	Glu	Arg	Asn	Arg	Ile	Arg	Lys	His	
				200					205					210	
Leu	Leu	Val	Phe	Ala	Leu	Ala	Ala	Pro	Val	Met	Ser	Met	Val	Thr	
				215					220					225	
Tyr	Leu	Gly	Leu	Ser	Lys	Ser	Ser	Lys	Glu	Ala	Leu	Ser	Glu	Val	

230	235	240
Asn Ala Thr Gly Val Ala Met Leu Phe	Ser Ala Gly Thr Phe	Leu
245	250	255
Tyr Val Ala Thr Val His Val Leu Pro	Glu Val Gly Gly Ile	Gly
260	265	270
His Ser His Lys Pro Asp Ala Thr Gly	Gly Arg Gly Leu Ser	Arg
275	280	285
Leu Glu Val Ala Ala Leu Val Leu Gly	Cys Leu Ile Pro Leu	Ile
290	295	300
Leu Ser Val Gly His Gln His		
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<210> 96
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 96
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<210> 97
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 97
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<210> 98
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 98
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<210> 99
 <211> 1429

<212> DNA
<213> Homo sapiens

<400> 99

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ctgattttga gatgatgggc ttgggaaacg ggcgtcgag catgaagtcg 150
ccgccccctg tgctggccgc cctggtggcc tgcattcatg tcttgggctt 200
caactactgg attgcgagct cccggagcgt ggacctccag acacggatca 250
tgagagctgga aggcagggtc cgcagggcgg ctgcagagag aggcgccgtg 300
gagctgaaga agaacgagtt ccaggagag ctggagaagc agcgggagca 350
gcttgacaaa atccagtcca gccacaactt ccagctggag agcgtcaaca 400
agctgtacca ggacgaaaag gcggttttgg tgaataacat caccacaggt 450
gagaggctca tccgagtgtc gcaagaccag ttaaagacct tgcagaggaa 500
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ggaatcatac actctgaatt gaactggaat cacatatttc acaacagggc 1350

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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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Leu	Val	Leu	Ala	Ala	Leu	Val	Ala	Cys	Ile	Ile	Val	Leu	Gly	Phe
				20					25					30

Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
				35					40					45

Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
				50					55					60

Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
				65					70					75

Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
				80					85					90

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
				95					100					105

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
				110					115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
				125					130					135

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
				140					145					150

Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
				155					160					165

Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
				170					175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
				185					190					195

Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
				200					205					210

Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
				215					220					225

Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
				230					235					240

Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr	245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu	260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val	275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro	290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met	305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu	320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu	335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser	350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile	365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu	380	385	390
Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu	395	400	

<210> 101
 <211> 3671
 <212> DNA
 <213> Homo sapiens

<400> 101
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 tgccatgggg gagccaaggg aaacctgggg cctgctggat ggcttcccga 200
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<210> 102
 <211> 1089
 <212> PRT
 <213> Homo sapiens

<400> 102
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 Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro
 35 40 45
 Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala
 50 55 60
 Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile
 65 70 75
 Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val
 80 85 90
 Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser
 95 100 105
 Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu
 110 115 120
 Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu
 125 130 135
 Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly
 140 145 150
 Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys
 155 160 165
 Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp
 170 175 180
 Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe
 185 190 195
 Phe Pro Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly

Ala	Tyr	Ala	Gly	Leu	Leu	Gly	Thr	Ile	Glu	Leu	Lys	Leu	Asp	Leu	
				500					505					510	
Val	Leu	Leu	Gly	Ala	Val	Ala	Ala	Val	Ser	Ser	Phe	Leu	Pro	Phe	
				515					520					525	
Leu	Trp	Lys	Ala	Trp	Ala	Gly	Trp	Gly	Ser	Lys	Arg	Pro	Leu	Ala	
				530					535					540	
Thr	Leu	Phe	Pro	Ile	Pro	Gly	Pro	Val	Leu	Leu	Leu	Leu	Leu	Phe	
				545					550					555	
Arg	Leu	Ala	Val	Phe	Phe	Ser	Asp	Ser	Phe	Val	Val	Ala	Glu	Ala	
				560					565					570	
Arg	Ala	Thr	Pro	Phe	Leu	Leu	Gly	Ser	Phe	Ile	Leu	Leu	Leu	Val	
				575					580					585	
Val	Gln	Leu	His	Trp	Glu	Gly	Gln	Leu	Leu	Pro	Pro	Lys	Leu	Leu	
				590					595					600	
Thr	Met	Pro	Arg	Leu	Gly	Thr	Ser	Ala	Thr	Thr	Asn	Pro	Pro	Arg	
				605					610					615	
His	Asn	Gly	Ala	Tyr	Ala	Leu	Arg	Leu	Gly	Ile	Gly	Leu	Leu	Leu	
				620					625					630	
Cys	Thr	Arg	Leu	Ala	Gly	Leu	Phe	His	Arg	Cys	Pro	Glu	Glu	Thr	
				635					640					645	
Pro	Val	Cys	His	Ser	Ser	Pro	Trp	Leu	Ser	Pro	Leu	Ala	Ser	Met	
				650					655					660	
Val	Gly	Gly	Arg	Ala	Lys	Asn	Leu	Trp	Tyr	Gly	Ala	Cys	Val	Ala	
				665					670					675	
Ala	Leu	Val	Ala	Leu	Leu	Ala	Ala	Val	Arg	Leu	Trp	Leu	Arg	Arg	
				680					685					690	
Tyr	Gly	Asn	Leu	Lys	Ser	Pro	Glu	Pro	Pro	Met	Leu	Phe	Val	Arg	
				695					700					705	
Trp	Gly	Leu	Pro	Leu	Met	Ala	Leu	Gly	Thr	Ala	Ala	Tyr	Trp	Ala	
				710					715					720	
Leu	Ala	Ser	Gly	Ala	Asp	Glu	Ala	Pro	Pro	Arg	Leu	Arg	Val	Leu	
				725					730					735	
Val	Ser	Gly	Ala	Ser	Met	Val	Leu	Pro	Arg	Ala	Val	Ala	Gly	Leu	
				740					745					750	
Ala	Ala	Ser	Gly	Leu	Ala	Leu	Leu	Leu	Trp	Lys	Pro	Val	Thr	Val	
				755					760					765	
Leu	Val	Lys	Ala	Gly	Ala	Gly	Ala	Pro	Arg	Thr	Arg	Thr	Val	Leu	
				770					775					780	
Thr	Pro	Phe	Ser	Gly	Pro	Pro	Thr	Ser	Gln	Ala	Asp	Leu	Asp	Tyr	

785										790				795			
Val	Val	Pro	Gln	Ile	Tyr	Arg	His	Met	Gln	Glu	Glu	Phe	Arg	Gly			
				800					805					810			
Arg	Leu	Glu	Arg	Thr	Lys	Ser	Gln	Gly	Pro	Leu	Thr	Val	Ala	Ala			
				815					820					825			
Tyr	Gln	Leu	Gly	Ser	Val	Tyr	Ser	Ala	Ala	Met	Val	Thr	Ala	Leu			
				830					835					840			
Thr	Leu	Leu	Ala	Phe	Pro	Leu	Leu	Leu	Leu	His	Ala	Glu	Arg	Ile			
				845					850					855			
Ser	Leu	Val	Phe	Leu	Leu	Leu	Phe	Leu	Gln	Ser	Phe	Leu	Leu	Leu			
				860					865					870			
His	Leu	Leu	Ala	Ala	Gly	Ile	Pro	Val	Thr	Thr	Pro	Gly	Pro	Phe			
				875					880					885			
Thr	Val	Pro	Trp	Gln	Ala	Val	Ser	Ala	Trp	Ala	Leu	Met	Ala	Thr			
				890					895					900			
Gln	Thr	Phe	Tyr	Ser	Thr	Gly	His	Gln	Pro	Val	Phe	Pro	Ala	Ile			
				905					910					915			
His	Trp	His	Ala	Ala	Phe	Val	Gly	Phe	Pro	Glu	Gly	His	Gly	Ser			
				920					925					930			
Cys	Thr	Trp	Leu	Pro	Ala	Leu	Leu	Val	Gly	Ala	Asn	Thr	Phe	Ala			
				935					940					945			
Ser	His	Leu	Leu	Phe	Ala	Val	Gly	Cys	Pro	Leu	Leu	Leu	Leu	Trp			
				950					955					960			
Pro	Phe	Leu	Cys	Glu	Ser	Gln	Gly	Leu	Arg	Lys	Arg	Gln	Gln	Pro			
				965					970					975			
Pro	Gly	Asn	Glu	Ala	Asp	Ala	Arg	Val	Arg	Pro	Glu	Glu	Glu	Glu			
				980					985					990			
Glu	Pro	Leu	Met	Glu	Met	Arg	Leu	Arg	Asp	Ala	Pro	Gln	His	Phe			
				995					1000					1005			
Tyr	Ala	Ala	Leu	Leu	Gln	Leu	Gly	Leu	Lys	Tyr	Leu	Phe	Ile	Leu			
				1010					1015					1020			
Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu	Ala	Ala	Ser	Ile	Leu	Arg			
				1025					1030					1035			
Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe	Ala	Pro	Lys	Phe	Ile	Phe			
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Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser	Val	Gly	Leu	Leu	Leu	Gly			
				1055					1060					1065			
Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly	Ala	Val	Ser	Ser	Trp	Phe			
				1070					1075					1080			

Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103
<211> 1743
<212> DNA
<213> Homo sapiens

<400> 103
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cttatccatc aacatgaaga atgtcctaca atggactcca ccagaggggtc 150
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgctc 250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350
taaatacaac agaacgtggt ccagtggtg gaccaaccac acgctgggtgc 400
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450
gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600
tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650
gattttgatt tatggaaatg aatttgaaa aagattcttt gtgcctgctg 700
aaaaaatcgt gattaacttt atcacctca atatctcgga tgattctaaa 750
atttctcatc aggatatgag tttactggga aaaagcagtg atgtatccag 800
ccttaatgat cctcagccca gcgggaacct gagggcccct caggaggaag 850
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900
gactctgaag aaaacacgga aggtacttct ctcaccacgc aagagtcctc 950
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcggt 1100
ggcagtcctg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc 1150
aagacttaga cccctggcg caggagcaca cagactcgga ggagggggcg 1200
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250

gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg 1300
agccttctga ggggggatggg ctcgagagagg agggctcttct atctagactc 1350
tatgaggagc cggctccaga caggccacca ggagaaaatg aaacctatct 1400
catgcaattc atggaggaat ggggggttata tgtgcagatg gaaaactgat 1450
gccaacactt ccttttgccct tttgtttcct gtgcaaacaa gtgagtcacc 1500
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ttgtcagtgt ctgtgagaat tacttatttc ttttctctat tctcatagca 1600
cgtgtgtgat tggttcatgc atgtaggctct cttaacaatg atgggtgggccc 1650
tctggagtcc aggggctggc cggttgttct atgcagagaa agcagtcaat 1700
aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

Met	Ser	Tyr	Asn	Gly	Leu	His	Gln	Arg	Val	Phe	Lys	Glu	Leu	Lys	1	5	10	15
Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu	20	25	30	
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr	35	40	45	
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser	50	55	60	
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu	65	70	75	
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His	80	85	90	
Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val	95	100	105	
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro	110	115	120	
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu	125	130	135	
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile	140	145	150	
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr	155	160	165	

Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	
				170					175					180	
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	
				185					190					195	
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	
				200					205					210	
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	
				215					220					225	
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	
				230					235					240	
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	
				245					250					255	
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	
				260					265					270	
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	
				275					280					285	
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	
				290					295					300	
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	
				305					310					315	
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	
				320					325					330	
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	
				335					340					345	
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	
				350					355					360	
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	
				365					370					375	
Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser	
				380					385					390	
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly	
				395					400					405	
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro	
				410					415					420	
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly	
				425					430					435	
Leu	Tyr	Val	Gln	Met	Glu	Asn									
				440											

<210> 105

<211> 21
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-21
 <223> Synthetic construct

 <400> 105
 cgctgctgct gttgctcctg g 21

 <210> 106
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 106
 cagtgtgccca ggactttg 18

 <210> 107
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 107
 agtcgcaggc agcgttgg 18

 <210> 108
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 108
 ctctccgag tctgtgtgct cctgc 25

 <210> 109
 <211> 51
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence

<222> 1-51
<223> Synthetic construct.

<400> 109
ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacad 50
c 51

<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 110
cggacgcgtg ggccggacgcg tgggcccgcg cgtgggtctc tgcggggaga 50
cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100
tctgtgact gtggccaccg ccctgatgct gcccgtaag cccccgcag 150
gctcctgggg ggccagatc atcgggggccc acgaggtgac cccccactcc 200
aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250
cttctgtctg cgagcccgtt ggggtggtctc ggccgcccac tgcttcagcc 300
acagagacct ccgactggc ctggtggtgc tgggcgccc cgtcctgagt 350
actgcggagc ccaccagca ggtgtttggc atcgatgctc tcaccacgca 400
ccccgactac caccatga cccacgcaa cgacatctgc ctgctgaggc 450
tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggctgcca 500
gggagaaggg ccaggcccc cacagcggg acacggtgcc ggggtggctgg 550
ctggggcttc gtgtctgact ttgaggagct gccgcctgga ctgatggagg 600
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cacctgacac ttaccatgct ctgcacccgc agtggggaca gccacagacg 700
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cccacgtgt acacgcagg gtccgccttt gtggcctgga tctgggacgt 850
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gccgtccag gcctggaatg ttccgtggct gggccccacg ggaagcctga 1000
tggtcagggg tgggggtggg cgggcagcgg tggggcacac ccattccaca 1050
tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met	Gly	Leu	Gly	Leu	Arg	Gly	Trp	Gly	Arg	Pro	Leu	Leu	Thr	Val	
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Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp	
				20					25					30	
Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg	
				35					40					45	
Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly	
				50					55					60	
Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys	
				65					70					75	
Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala	
				80					85					90	
His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile	
				95					100					105	
Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala	
				110					115					120	
Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly	
				125					130					135	
Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro	
				140					145					150	
Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val	
				155					160					165	
Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val	
				170					175					180	
Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His	
				185					190					195	
Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg	
				200					205					210	
Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg	
				215					220					225	
Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly	
				230					235					240	
Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val	
				245					250					255	

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
 260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
 275 280

<210> 112
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 112
 gacgtctgca acagctcctg gaag 24

<210> 113
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 113
 cgagaaggaa acgaggccgt gag 23

<210> 114
 <211> 44
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-44
 <223> Synthetic construct.

<400> 114
 tgacacttac catgctctgc acccgcagtg gggacagcca caga 44

<210> 115
 <211> 1808
 <212> DNA
 <213> Homo sapiens

<400> 115
 gagctaccca ggcggctggt gtgcagcaag ctccgcgccg actccggacg 50
 cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100
 cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150
 tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200

ggatcatcgtg acgggacgcca acacaggcat cgggaagcag accgccttgg 250
 aactggccag gagaggagc aacatcatcc tggcctgccg agacatggag 300
 aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350
 tgtcaacgcc cggcacctgg acttggttc cctcaagtct atccgagagt 400
 ttgcagcaaa gatcattgaa gaggaggagc gagtggacat tctaataaac 450
 aacgcggtg tgatgcgtg cccactgg accaccgagg acggcttoga 500
 gatgcagttt ggcgttaacc acctgggtca ctttctcttg acaaacttgc 550
 tgctggacaa gctgaaagcc tcagcccctt cgcggatcat caacctctcg 600
 tccctggccc atgttgctgg gcacatagac tttgacgact tgaactggca 650
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 gtctctctg agccttggtt tcttcagcag tgagatgctc agaataactg 1550
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 ggctgtgccg ggggtgtttg ctgagggctt cctgtgccag agcccagcca 1650

gagagcaggt gcaggtgtca tcccgagttc aggctctgca cggcatggag 1700
 tggaaccccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750
 caccttccta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800
 gctcattt 1808

<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116
 Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala
 1 5 10 15
 Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys
 20 25 30
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
 50 55 60
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
 65 70 75
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
 80 85 90
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
 95 100 105
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
 110 115 120
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
 125 130 135
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
 140 145 150
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
 155 160 165
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
 170 175 180
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
 185 190 195
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
 200 205 210
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
 215 220 225

Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230					235					240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117
 <211> 2249
 <212> DNA
 <213> Homo sapiens

<400> 117
 gaagttcgcg agcgcctggca tgtggtcctg gggcgcggtt ggcggcgctg 50
 ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100
 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccc 150
 agcgccggct gctggggctg ctgaggcggc acctgcgcgg ggaggaggcg 200
 cggctgcggg acctgactag attctacgac aaggtacttt ctttgcata 250
 ggattcaaca acccctgtgg ctaaccctct gcttgcatat actctcatca 300
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
 gagaacatcc gagctctgaa ggatggctat gagaaggtgg agcaagacct 400
 tccagccttt gaggaccttg agggagcagc aagggccctg atgcggctgc 450
 aggacgtgta catgctcaat gtgaaaggcc tggcccgagg tgtctttcag 500
 agagtcaact gctctgccat cactgacctg tacagcccca aacggctctt 550
 ttctctcaca ggggatgact gcttccaagt tggcaagggt gcctatgaca 600
 tgggggatta ttaccatgcc attccatggc tggaggaggc tgtcagtctc 650
 ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700

tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
1 5 10 15

Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr
20 25 30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

Gly	Asn	Val	Ser	Cys	Ala	Leu	Ser	Leu	Ser	Arg	Glu	Phe	Leu	Leu	
				245					250					255	
Tyr	Ser	Pro	Asp	Asn	Lys	Arg	Met	Ala	Arg	Asn	Val	Leu	Lys	Tyr	
				260					265					270	
Glu	Arg	Leu	Leu	Ala	Glu	Ser	Pro	Asn	His	Val	Val	Ala	Glu	Ala	
				275					280					285	
Val	Ile	Gln	Arg	Pro	Asn	Ile	Pro	His	Leu	Gln	Thr	Arg	Asp	Thr	
				290					295					300	
Tyr	Glu	Gly	Leu	Cys	Gln	Thr	Leu	Gly	Ser	Gln	Pro	Thr	Leu	Tyr	
				305					310					315	
Gln	Ile	Pro	Ser	Leu	Tyr	Cys	Ser	Tyr	Glu	Thr	Asn	Ser	Asn	Ala	
				320					325					330	
Tyr	Leu	Leu	Leu	Gln	Pro	Ile	Arg	Lys	Glu	Val	Ile	His	Leu	Glu	
				335					340					345	
Pro	Tyr	Ile	Ala	Leu	Tyr	His	Asp	Phe	Val	Ser	Asp	Ser	Glu	Ala	
				350					355					360	
Gln	Lys	Ile	Arg	Glu	Leu	Ala	Glu	Pro	Trp	Leu	Gln	Arg	Ser	Val	
				365					370					375	
Val	Ala	Ser	Gly	Glu	Lys	Gln	Leu	Gln	Val	Glu	Tyr	Arg	Ile	Ser	
				380					385					390	
Lys	Ser	Ala	Trp	Leu	Lys	Asp	Thr	Val	Asp	Pro	Lys	Leu	Val	Thr	
				395					400					405	
Leu	Asn	His	Arg	Ile	Ala	Ala	Leu	Thr	Gly	Leu	Asp	Val	Arg	Pro	
				410					415					420	
Pro	Tyr	Ala	Glu	Tyr	Leu	Gln	Val	Val	Asn	Tyr	Gly	Ile	Gly	Gly	
				425					430					435	
His	Tyr	Glu	Pro	His	Phe	Asp	His	Ala	Thr	Ser	Pro	Ser	Ser	Pro	
				440					445					450	
Leu	Tyr	Arg	Met	Lys	Ser	Gly	Asn	Arg	Val	Ala	Thr	Phe	Met	Ile	
				455					460					465	
Tyr	Leu	Ser	Ser	Val	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr	
				470					475					480	
Ala	Asn	Leu	Ser	Val	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp	
				485					490					495	
Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His	
				500					505					510	
Ala	Gly	Cys	Pro	Val	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys	
				515					520					525	
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser	

Ser Pro Glu Asp

<210> 119

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 119

cgggacagga gacccagaaa ggg 23

<210> 120

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 120

ggccaagtga tccaaggcat cttc 24

<210> 121

<211> 49

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-49

<223> Synthetic construct.

<400> 121

ctgcgggacc tgactagatt ctacgacaag gtactttcct tgcattgggg 49

<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens

<400> 122

gagataggga gtctgggttt aagttcctgc tccatctcag gagccccctgc 50

tcccaccctt aggaagccac cagactccac ggtgtggggc caatcagggtg 100

gaatcggccc tggcagggtg ggccacgagc gctggctgag ggaccgagcc 150

ggagagcccc ggagcccccg taaccgcgcg ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250
gctcaagttt tcactttatca tctattccac cgtgttctgg ctgattgggg 300
ccctggtcct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350
aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcctcctcct 400
gggcgtcgtc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450
gtgacaacct gtacottctc caagcattca tgtacatcct tgggatctgc 500
ctcatcatgg agctcattgg tggcgtgggt gccttgacct tccggaacca 550
gaccattgac ttctgaacg acaacattcg aagaggaatt gagaactact 600
atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650
aagtgtgtg gcggggagga ctaccgagat tggagcaaga atcagtacca 700
cgactgcagt gcccctggac ccctggcctg tggggtgccc tacacctgct 750
gcatcaggaa cacgacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800
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gcatcctcct gggcatcctg cttcccagc tcctgggggt gctgctgacg 950
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tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700
 gtcttattct tgcccttccc ccaaccagtt tgtaatacaa acaataaaaa 1750
 catgttttgt tttgttttta aaaaaaaa 1778

<210> 123
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 123
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 1 5 10 15
 Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
 20 25 30
 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala
 35 40 45
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
 50 55 60
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met
 65 70 75
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
 80 85 90
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
 95 100 105
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
 110 115 120
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
 125 130 135
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
 140 145 150
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
 155 160 165
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly
 170 175 180
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn
 185 190 195
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val
 200 205 210
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile
 215 220 225
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu Tyr	
245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp	
260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly	
275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn		
290		

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 124
 atcatctatt ccaccgtgtt ctggc 25

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 125
 gacagagtgc tccatgatga tgtcc 25

<210> 126
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 126
 cctgtctgtg ggcatttatg cagaggtga gcggcagaaa tataaaaccc 50

<210> 127
 <211> 1636
 <212> DNA
 <213> Homo sapiens

<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcaatt 50
gctgccctct gacacctggg aagatggccg gcccgtaggac cttcaccctt 100
ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtccac 150
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
ggtgaacacc gtcctgaagc acatcatctg gctgaaggct atcacagcta 350
acatcctcca gctgcagggt aagccctcgg ccaatgacca ggagctgcta 400
gtcaagatcc ccttgacat ggtggctgga ttcaacacgc ccctggtcaa 450
gaccatcgtg gagttccaca tgacgactga ggcccaagcc accatccgca 500
tggaacaccag tgcaagtggc cccaccgcgc tggtcctcag tgactgtgcc 550
accagccatg ggagcctgcg catccaactg ctgtataagc tctccttctt 600
ggtgaacgcc ttagctaagc aggtcatgaa cctcctagtg ccatccctgc 650
ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat 700
ggcatgtatg cagacctcct gcagctgggt aaggtgcca tttccctcag 750
cattgaccgt ctggagtttg accttctgta tctgccatc aagggtgaca 800
ccattcagct ctacctgggg gccaaagtgt tggactcaca gggaaagggtg 850
accaagtgtt tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900
caacatcccg ttcagcctca tcgtgagtca ggacgtgggt aaagctgcag 950
tggctgctgt gctctctcca gaagaattca tggtcctggt ggactctgtg 1000
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accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350
cactgagatc atccactcca tcctgtgcc gaaccagaat ggcaaattaa 1400
gatctgggggt cccagtgtca ttggtgaagg ccttgggatt cgaggcagct 1450

gagtcctcac tgaccaagga tgcccttggtg cttactccag cctccttggtg 1500
gaaacccagc tctcctgtct cccagtgaag acttggtgag cagccatcag 1550
ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600
cctctctgca atcaataaac acttgccctgt gaaaaa 1636

<210> 128
<211> 484
<212> PRT
<213> Homo sapiens

<400> 128
Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala
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Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile
20 25 30
Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys
35 40 45
Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
50 55 60
Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
65 70 75
Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
80 85 90
Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
95 100 105
Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
110 115 120
Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
125 130 135
Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
140 145 150
Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
155 160 165
Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu
170 175 180
Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu
185 190 195
Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly
200 205 210
Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu
215 220 225

Ser	Ile	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys	230	235	240
Gly	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser	245	250	255
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu	260	265	270
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser	275	280	285
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu	290	295	300
Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His	305	310	315
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp	320	325	330
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr	335	340	345
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu	350	355	360
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu	365	370	375
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr	380	385	390
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp	395	400	405
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp	410	415	420
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu	425	430	435
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu	440	445	450
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys	455	460	465
Asp	Ala	Leu	Val	Leu	Thr	Pro	Ala	Ser	Leu	Trp	Lys	Pro	Ser	Ser	470	475	480
Pro Val Ser Gln																	

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens


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<400> 129
gagcgaacat ggcagcgcgt tggcgggtttt ggtgtgtctc tgtgaccatg 50
gtggtggcgc tgctcatcgt ttgcgacgtt ccctcagcct ctgccccaaag 100
aaagaaggag atggtgttat ctgaaaagggt tagtcagctg atggaatgga 150
ctaacaaaag acctgtaata agaataaatg gagacaagtt ccgtcgcctt 200
gtgaaagccc caccgagaaa ttactcogtt atcgtcatgt tcaactgctct 250
ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300
agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350
ttttttgcca tgggtggattt tgatgaaggc tctgatgtat ttcagatgct 400
aaacatgaat tcagctccaa ctttcatcaa ctttcctgca aaagggaaac 450
ccaaacgggg tgatacatat gagttacagg tgcgggggttt ttcagctgag 500
cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550
tagacccccca aattatgctg gtccccttat gttgggattg cttttggctg 600
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ctttctgatg agttaaaaag gtcccagaga tatatagaca ctggagtact 1050
ggaaattgaa aaacgaaaat cgtgtgtgtt tgaaaagaag aatgcaactt 1100
gtatatatttg tattacctct ttttttcaag tgattttaa atgttaatcat 1150
ttaaccaaag aagatgtgta gtgccttaac aagcaatcct ctgtcaaaaat 1200
ctgaggtatt tgaaaataat tatectctta accttctctt cccagtgaac 1250
tttatggaac atttaattta gtacaattaa gtatattata aaaattgtaa 1300
aactactact ttgttttagt tagaaciaag ctcaaaaacta ctttagtta 1350
cttggtcatc tgattttata ttgccttacc caaagatggg gaaagtaagt 1400
cctgaccagg tgttcccaca tatgcctgtt acagataact acattaggaa 1450

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ttcattotta gcttcttcat ctttgtgtgg atgtgtatac tttacgcac 1500
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 gaacaccatt cttcagagca cacgtctagc cctcagcaag acagtgtgtt 1600
 ctctctctcc ttgcatatct cctactgcgc tccagcctga gtgatagagt 1650
 gagactctgt ctcaaaaaaa agtatctcta aatacaggat tataatttct 1700
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 tcagcacttt gggaggccaa ggcaggcaga tcacgaggtc aggagttcga 2000
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 aaaaaaaaaaaa aaa 2213

<210> 130
 <211> 335
 <212> PRT
 <213> Homo sapiens

<400> 130
 Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val
 1 5 10 15
 Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln
 20 25 30
 Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met
 35 40 45
 Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
 50 55 60
 Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
 65 70 75
 Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
 80 85 90
 Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
 95 100 105

Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp	
				110					115					120	
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser	
				125					130					135	
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg	
				140					145					150	
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln	
				155					160					165	
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val	
				170					175					180	
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu	
				185					190					195	
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met	
				200					205					210	
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys	
				215					220					225	
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg	
				230					235					240	
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn	
				245					250					255	
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His	
				260					265					270	
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu	
				275					280					285	
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys	
				290					295					300	
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser	
				305					310					315	
Trp	Met	Leu	Ser	Ile	Phe	Arg	Ser	Lys	Tyr	His	Gly	Tyr	Pro	Tyr	
				320					325					330	
Ser	Phe	Leu	Met	Ser											
				335											

<210> 131

<211> 2476

<212> DNA

<213> Homo sapiens

<400> 131

aagcaaccaa actgcaagct ttgggagttg ttgctgtcc ctgccctgct 50

ctgctaggga gagaacgcca gagggaggcg gctggccogg cggcaggctc 100

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 cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200
 cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250
 aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300
 ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350
 caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
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 aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550
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 ttcaccatct tctggagaaa attttgatc ttcaacattt cacacatctc 800
 tttattggct tgaaaaagtg tctcatgatg ccatcaaaat cccaaagtgg 850
 tcacctttgt cagaaatgca ccctgtagat tattactctt cttatacaaa 900
 aaactgcact ggaagattta caaaaaaaga aattaagaat attagagcat 950
 tttattatgc tatgtgtgct gagacagatg ccatgcttgg tgaaattatt 1000
 ttggcccttc atcaattaga tcttcttcag aaaactattg tcatatactc 1050
 ctcagaccat ggagagctgg ccatggaaca tcgacagttt tataaaatga 1100
 gcatgtacga ggctagtgc catgttccgc ttttgatgat gggaccagga 1150
 attaaagccg gcctacaagt atcaaagtgt gtttctcttg tggaatttta 1200
 ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagt 1250
 gatactcttt gttgccgtta tcatcagaaa catttaagaa tgaacataaa 1300
 gtcaaaaacc tgcatccacc ctggattctg agtgaattcc atggatgtaa 1350
 tgtgaatgcc tccacctaca tgcttcgaac taaccactgg aaatatatag 1400
 cctattcgga tggatcatca atattgcctc aactctttga tctttcctcg 1450
 gatccagatg aattaacaaa tgttgctgta aaatttcag aaattactta 1500
 ttctttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550


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otttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600
ataggacaga attattcaaa cgttatagca aatcttaggt ggcaccaaga 1650
ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700
aaacccatat gaatccaaga gcagtttgaa caaaaagttt aaaaatagt 1750
ttctagagat acatataaat atattacaag atcataatta tgtattttta 1800
atgaaacagt ttttaataatt accaagtttt ggccgggcac agtgggtcac 1850
acctgtaatc ccaggacttt gggaggctga ggaaagcaga tcacaaggtc 1900
aagagattga gaccatcctg gccaacatgg tgaaaccctg tctctactaa 1950
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agtgaagtga gattgcgcca ctgtactcca gcctggcaac agagtgagac 2100
tgtgtcgcaa aaaaataaaa ataaaataat aataattacc aatttttcat 2150
tattttgtaa gaatgtagtg tattttaaga taaaatgcca atgattataa 2200
aatcacatat tttcaaaaat ggttattatt taggcctttg tacaatttct 2250
aacaatttag tggaagtatc aaaaggattg aagcaaatac tgtaacagtt 2300
atgttccttt aaataataga gaatataaaa tattgtaata atatgtatca 2350
taaaatagtt gtatgtgagc atttgatggt gaaaaaaaaa aaaaaaaaaa 2400
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<210> 132
<211> 536
<212> PRT
<213> Homo sapiens

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<400> 132
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 1             5             10             15
Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys
          20             25             30
Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
          35             40             45
Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
          50             55             60
Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
          65             70             75

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Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	
				260					265					270	
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	
				275					280					285	
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	
				290					295					300	
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	
				305					310					315	
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	
				320					325					330	
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	
				335					340					345	
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	
				350					355					360	
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn	

Leu	Ser	Gly	Tyr	Ser	Leu	Leu	Pro	Leu	Ser	Ser	Glu	Thr	Phe	Lys
				380					385					390
Asn	Glu	His	Lys	Val	Lys	Asn	Leu	His	Pro	Pro	Trp	Ile	Leu	Ser
				395					400					405
Glu	Phe	His	Gly	Cys	Asn	Val	Asn	Ala	Ser	Thr	Tyr	Met	Leu	Arg
				410					415					420
Thr	Asn	His	Trp	Lys	Tyr	Ile	Ala	Tyr	Ser	Asp	Gly	Ala	Ser	Ile
				425					430					435
Leu	Pro	Gln	Leu	Phe	Asp	Leu	Ser	Ser	Asp	Pro	Asp	Glu	Leu	Thr
				440					445					450
Asn	Val	Ala	Val	Lys	Phe	Pro	Glu	Ile	Thr	Tyr	Ser	Leu	Asp	Gln
				455					460					465
Lys	Leu	His	Ser	Ile	Ile	Asn	Tyr	Pro	Lys	Val	Ser	Ala	Ser	Val
				470					475					480
His	Gln	Tyr	Asn	Lys	Glu	Gln	Phe	Ile	Lys	Trp	Lys	Gln	Ser	Ile
				485					490					495
Gly	Gln	Asn	Tyr	Ser	Asn	Val	Ile	Ala	Asn	Leu	Arg	Trp	His	Gln
				500					505					510
Asp	Trp	Gln	Lys	Glu	Pro	Arg	Lys	Tyr	Glu	Asn	Ala	Ile	Asp	Gln
				515					520					525
Trp	Leu	Lys	Thr	His	Met	Asn	Pro	Arg	Ala	Val				
				530					535					

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 133
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 tcaaggagca agagcttcag cctgaagaca agggagcagt ccctgaagac 100
 gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150
 ctacatccta ggccttcttg ggcttttggg cacactgggt gccatgctgc 200
 tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
 gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300
 catcaccagc tgtgacatct atagcaccct tctgggcctg cccgctgaca 350
 tccaggctgc ccaggccatg atggtgacat ccagtgaat ctctccctg 400
 gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atccccgagcc aaagacagag tggcggttagc aggtggagtc tttttcatcc 500
 ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggatc 550
 ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600
 tggagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650
 ctggaatcat cctctgcttt tctgtctcat cccagagaaa tcgctccaac 700
 tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750
 gcctggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800
 cagggatatgt gtgaagaacc agggggccaga gctgggggggt ggctgggtct 850
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 actggatcgt gtcagaagggt gctgctgagg atagactgac tttggccatt 950
 ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000
 attgccaagg atgctcgcca tgccagcctt tctgttttcc tcaccttgct 1050
 gctccctgc cctaagtccc caacctcaa cttgaaacct cattccctta 1100
 agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150
 ccccaaaccc actaatcaca tccactgac tgaccctctg tgatcaaaga 1200
 ccctctctct ggctgaggtt ggctcttagc tcattgctgg ggatgggaag 1250
 gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300
 cctccaaaga aactgattgg ccctggaacc tccatccac tcttgttatg 1350
 actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400
 tacggtatcc agggaacaga aagcaggatg caggatggga ggacaggaag 1450
 gcagcctggg acatttaaaa aaata 1475

<210> 134
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 134
 Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
 1 5 10 15
 Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp
 20 25 30
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
 35 40 45
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

Ile Thr Gln Cys Asp	Ile Tyr Ser Thr	Leu Leu Gly Leu Pro Ala
65	70	75
Asp Ile Gln Ala Ala	Gln Ala Met Met	Val Thr Ser Ser Ala Ile
80	85	90
Ser Ser Leu Ala Cys	Ile Ile Ser Val	Val Gly Met Arg Cys Thr
95	100	105
Val Phe Cys Gln Glu	Ser Arg Ala Lys	Asp Arg Val Ala Val Ala
110	115	120
Gly Gly Val Phe Phe	Ile Leu Gly Gly	Leu Leu Gly Phe Ile Pro
125	130	135
Val Ala Trp Asn Leu	His Gly Ile Leu	Arg Asp Phe Tyr Ser Pro
140	145	150
Leu Val Pro Asp Ser	Met Lys Phe Glu	Ile Gly Glu Ala Leu Tyr
155	160	165
Leu Gly Ile Ile Ser	Ser Leu Phe Ser	Leu Ile Ala Gly Ile Ile
170	175	180
Leu Cys Phe Ser Cys	Ser Ser Gln Arg	Asn Arg Ser Asn Tyr Tyr
185	190	195
Asp Ala Tyr Gln Ala	Gln Pro Leu Ala	Thr Arg Ser Ser Pro Arg
200	205	210
Pro Gly Gln Pro Pro	Lys Val Lys Ser	Glu Phe Asn Ser Tyr Ser
215	220	225
Leu Thr Gly Tyr Val		
230		

<210> 135
 <211> 610
 <212> DNA
 <213> Homo sapiens

<400> 135
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 aagtcacgcg tcccgtggc tcagaaccat ggctgtgcca gccggcacc 150
 aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200
 cgccatcgtg tccctgagcg agaccgcga atgtggtccc ccctgcacct 250
 tctggccctg ctttgagctc tgctgtcttg attcctttgg cctcacaaac 300
 gattttgttg tgaagctgaa ggttcagggt gtgaattccc agtgccactc 350

atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
 atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600
 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
 1 5 10 15
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
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 gtcttttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100
 agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

ctgctttgag cagtgtgcc cctggacctt catggtgaag ctgataaacc 300
agaactgcga ctcagccccg acctcggatg acaggctttg tcgcagtgtc 350
agctaattgga acatcagggg aacgatgact cctggattct ccttcctggg 400
tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450
gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500
gacctgtctg agggccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550
ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600
ggactctgaa ccctcctgat gaccctatg gccaacatca acccggcacc 650
acccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700
atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750
tatgtacttt ataaatgaaa a 771

<210> 138
<211> 110
<212> PRT
<213> Homo sapiens

<400> 138
Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys
1 5 10 15
Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met
20 25 30
Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp
35 40 45
Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val
50 55 60
Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg
65 70 75
Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu
80 85 90
Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu
95 100 105
Cys Arg Ser Val Ser
110

<210> 139
<211> 2044
<212> DNA
<213> Homo sapiens

<400> 139

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 gctcgcactc agtcgcgga ggcttccccg cgcgggcgc gtcccgcccg 100
 ctccccggca ccagaagttc ctctgcgct ccgacggcga catgggcgtc 150
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgccttctgc 200
 tctcttctg gctgcgtccc taggtccgtt ggagccttc aaggtcgcca 250
 cgccgtattc cctgtatgtc tgtcccgagg ggagaaacgt caccctcacc 300
 tgcaggctct tgggccctgt ggacaaaggg cagcatgtga ccttctacaa 350
 gacgtggtac cgcagctcga ggggcgaggt gcagacctgc tcagagcgcc 400
 ggcccatccg caacctcag ttccaggacc ttcacctgca ccatggaggc 450
 caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500
 gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550
 ccctgctgga tagcggcctc tactgctgcc tgggtgtgga gatcaggcac 600
 caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650
 aggcaaagat gcaccatcca actgtgtggt gtacccatcc tcctcccagg 700
 atagtgaana catcacggct gcagccctgg ctacgggtgc ctgcatcgta 750
 ggaatcctct gcctccccct catcctgctc ctggtctaca agcaaaggca 800
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 ttcaagggat tgaanaaaaa ggctttgaag cctcaccacc tgcccagggg 900
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 gccttctgag tctgggcggc atctgcttcc ggagcccagc accccctgt 1000
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 gactctcaa actttgaggt catctagccc agctggggga cagtgggctg 1100
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 gatactgtga catccagaa gccagcccc tcaaccctc tggatgctac 1250
 atggggatgc tggacggctc agccctgtt ccaaggattt tggggtgctg 1300
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 gttgccccac ccactggaga tggtgctgag ggaggtgggt ggggccttct 1850
 gggaaggtga gtggagaggg gcacctgccc cccgccctcc ccatccccta 1900
 ctcccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950
 ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 140
 Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly
 1 5 10 15
 Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val
 20 25 30
 Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro
 35 40 45
 Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val
 50 55 60
 Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser
 65 70 75
 Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg
 80 85 90
 Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln
 95 100 105
 Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu
 110 115 120
 Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn
 125 130 135
 Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

140 145 150

Ile	Arg	His	His	His	Ser	Glu	His	Arg	Val	His	Gly	Ala	Met	Glu
				155					160					165
Leu	Gln	Val	Gln	Thr	Gly	Lys	Asp	Ala	Pro	Ser	Asn	Cys	Val	Val
				170					175					180
Tyr	Pro	Ser	Ser	Ser	Gln	Asp	Ser	Glu	Asn	Ile	Thr	Ala	Ala	Ala
				185					190					195
Leu	Ala	Thr	Gly	Ala	Cys	Ile	Val	Gly	Ile	Leu	Cys	Leu	Pro	Leu
				200					205					210
Ile	Leu	Leu	Leu	Val	Tyr	Lys	Gln	Arg	Gln	Ala	Ala	Ser	Asn	Arg
				215					220					225
Arg	Ala	Gln	Glu	Leu	Val	Arg	Met	Asp	Ser	Asn	Ile	Gln	Gly	Ile
				230					235					240
Glu	Asn	Pro	Gly	Phe	Glu	Ala	Ser	Pro	Pro	Ala	Gln	Gly	Ile	Pro
				245					250					255
Glu	Ala	Lys	Val	Arg	His	Pro	Leu	Ser	Tyr	Val	Ala	Gln	Arg	Gln
				260					265					270
Pro	Ser	Glu	Ser	Gly	Arg	His	Leu	Leu	Ser	Glu	Pro	Ser	Thr	Pro
				275					280					285
Leu	Ser	Pro	Pro	Gly	Pro	Gly	Asp	Val	Phe	Phe	Pro	Ser	Leu	Asp
				290					295					300
Pro	Val	Pro	Asp	Ser	Pro	Asn	Phe	Glu	Val	Ile				
				305					310					

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 cttagacctc ctttctgcc ctcttttctt gccacogct gtttctggc 150
 ccttctccga ccccgctcta gcagcagacc tctgggggtc tgtgggttga 200
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact 250
 ccgctcccgg accagcggcc tgaccctggg gaaaggatgg ttcccgaggt 300
 gagggctctc tcttcttgc tgggactcgc gctgctctgg ttccccctgg 350
 actcccacgc tcgagccgc ccagacatgt tctgcctttt ccatgggaag 400
 agatactccc ccggcgagag ctggcacccc tacttggagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500
accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550
cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600
ggccccacca aagtcttgcc agcacaacgg gaccatgtac caacacggag 650
agatcttcag tgcccatgag ctgttccctt cccgcctgcc caaccagtgt 700
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750
ccccgaacca ggctgcccag caccctctcc actgccagac tcctgctgcc 800
aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850
cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900
tgggagaaag agaggcccgg gcaccccagc cccactggc ctcagcgccc 950
ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000
actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050
cgggaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100
tcggcccctt gccctgcac ctatgcacct gtgaggatgg ccgccaggac 1150
tgccagcgtg tgacctgtcc caccgagtac cctgcccgtc accccgagaa 1200
agtggctggg aagtgtgca agatttgccc agaggacaaa gcagaccctg 1250
gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
ctcgtccaca catcggtatc cccaagccca gacaacctgc gtcgctttgc 1350
cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg 1400
taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450
ccacacagcc agaattctcc acttgactca gatcaagaaa gtcaggaagc 1500
aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550
gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600
ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650
gatatgagct gtataattgt tgttattata tattaataaa taagaagttg 1700
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142
<211> 451
<212> PRT
<213> Homo sapiens
<400> 142

Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala	1	5	10	15
Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp	20	25	30	
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser	35	40	45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg	50	55	60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His	65	70	75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln	80	85	90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg	95	100	105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His	110	115	120	
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	125	130	135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	140	145	150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	155	160	165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	170	175	180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	185	190	195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	200	205	210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	215	220	225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	230	235	240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	245	250	255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	260	265	270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	275	280	285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys				

290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys	Cys Cys Lys Ile Cys Pro	
305	310	315
Glu Asp Lys Ala Asp Pro Gly His Ser	Glu Ile Ser Ser Thr Arg	
320	325	330
Cys Pro Lys Ala Pro Gly Arg Val Leu	Val His Thr Ser Val Ser	
335	340	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe	Ala Leu Glu His Glu Ala	
350	355	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp	Lys Leu Val Lys Asp Glu	
365	370	375
Glu Thr Glu Ala Gln Arg Gly Glu Val	Pro Gly Pro Arg Pro His	
380	385	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp	Gln Glu Ser Gln Glu Ala	
395	400	405
Arg Leu Pro Glu Arg Gly Thr Ala Leu	Pro Thr Ala Arg Trp Pro	
410	415	420
Pro Arg Arg Ser Leu Glu Arg Leu Pro	Ser Pro Asp Pro Gly Ala	
425	430	435
Glu Gly His Gly Gln Ser Arg Gln Ser	Asp Gln Asp Ile Thr Lys	
440	445	450

Thr

<210> 143
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 143
 ctacgctgcg ccaaggggta gtgagaccgc gcggaacag cttgcggctg 50
 cgaggagctc ccgtgggcgc tccgctggct gtgcaggcgg ccatggattc 100
 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150
 tgggctacgc gctcctcggt atcgtgaccc cgaggagcgc gcggaagcag 200
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
 ggcaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300
 cgcaggagaa cgtggcctgg aggaagaact ggatgggttg cggcgaaggc 350
 ggcgccagcg ggaggtcacc gtgagaccgc acttgccctc gtgggcgcgc 400
 gaccttggtt tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct cgggggtcct 500
 gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550
 ttttaaggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
 1 5 10 15
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 50 55 60
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
 80 85 90
 Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
 caggagagaa ggcaccgccc ccaccccgcc tccaaagcta accctcgggc 50
 ttgaggggaa gaggctgact gtacgttcct tctactctgg caccactctc 100
 caggctgccca tggggcccag caccctctc ctcatcttgt tccttttgtc 150
 atggtcggga cccctccaag gacagcagca ccaccttggt gagtacctg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350
 acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagacccaga accagctct gccctgtgta gagtttgatg agaaggtgac 450
tggaggccct gggaccaaag gcaaggaag aaggaatgag aagtacgata 500
tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550
ctgaagcgat ttggtggccc agctgggtcta tggaccaagg atccactggg 600
gcaaacagag aagatctacg tgtagatgg gacacagaat gacacagcct 650
ttgtcttccc aaggctgctg gacttcaccc ttgccatggc tgcccggaaa 700
gcttcccagag tccgggtgcc cttcccctgg gtaggcacag ggcagctggt 750
atatggtggc tttctttatt ttgctcggag gcctcctgga agacctggtg 800
gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850
aaccgaacag tgggtggacag ctcagtattc ccagcagagg ggctgatccc 900
cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950
aaggtctttg ggctgtctat gccaccggg aggatgacag gcacttgtgt 1000
ctggccaagt tagatccaca gacctggac acagagcagc agtgggacac 1050
accatgtccc agagagaatg ctgaggctgc ctttgtcatc tgtgggaccc 1100
tctatgtcgt ctataacacc cgtcctgcca gtcggggccc catccagtgc 1150
tcctttgatg ccagcggcac cctgaccct gaacgggcag cactccctta 1200
ttttcccgc agatatggtg cccatgccag cctccgctat aacccccgag 1250
aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300
gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350
catctttctc actcccatc atttatatta tatccccact aaatttcttg 1400
ttctcattc ttcaaagtg ggccagttgt ggctcaaata ctctatatatt 1450
ttagccaatg gcaatcaaat tctttcagct cctttgtttc atacggaact 1500
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cccagaccca gggctctaac cttgtatgcg ggcaggccca gggagcaggc 1650
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acgtccagct ctgtcctctc ttctcactc ctcccttcag tgtcctgagg 1750
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gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
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Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20					25					30
Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35					40					45
Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
				50					55					60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
				65					70					75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
				80					85					90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
				95					100					105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
				110					115					120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
				125					130					135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
				140					145					150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
				155					160					165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
				170					175					180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
				185					190					195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
				200					205					210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
				215					220					225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
				230					235					240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
				245					250					255

Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala	
				260					265					270	
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala	
				275					280					285	
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys	
				290					295					300	
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro	
				305					310					315	
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr	
				320					325					330	
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile	
				335					340					345	
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala	
				350					355					360	
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu	
				365					370					375	
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly	
				380					385					390	
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu	
				395					400					405	

Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
 gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgcctt 50
 ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca 100
 gttctcctct tctctctaata ccatccgtca cctctcctgt catccgtttc 150
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgttttg 250
 gccagacaag cctgtccagg ccttgggtgg ggaggacgca gcattctcct 300
 gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
 attctattgc ggagggggcg atctctctga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
 gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600
 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650
 tcgggctggg tccccggcc cacagcgaag tggaaaggct cacaaggaca 700
 ggatttgtcc acagactcca ggacaaacag agacatgcat ggctgtttg 750
 atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800
 tccatgcggc atgctcatct gagccgagag gtggaatcca gggtacagat 850
 aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900
 tgggaatact ctgctgtggc ctattttttg gcattgttgg actgaagatt 950
 ttcttctcca aattccagtg gaaaatccag gcggaactgg actggagaag 1000
 aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg 1050
 tgactctgga tccagagacg gtcacccga agctctgcgt ttctgatctg 1100
 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150
 gagatttaca aggaagagtg tgggtggctt tcagagtttc caagcaggga 1200
 aacattactg ggaggtggac ggaggacaca ataaaagggtg gcgcgtggga 1250
 gtgtgccggg atgatgtgga caggaggaag gactacgtga ctttgtctcc 1300
 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350
 cattaaatcc ccgttttatc agcgtcttcc ccaggacccc acctacaaaa 1400
 ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450
 aaatgaccag tcccttattt ataccctgac atgtcggttt gaaggcttat 1500
 tgaggcccta cattgagtat ccgtcctata atgagcaaaa tggaactccc 1550
 atagtcatct gccagtcac ccaggaatca gagaaaggag cctcttggca 1600
 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650
 caaccacgcc ctctctcccc aggggtgaaa tgtaggatga atcacatccc 1700
 acattcttct ttagggatat taaggctctc ctcccagatc caaagtcccg 1750
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 atgggagtca ggtgtcatgg ctgccctgag ctgggaggga agaaggctga 1850
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 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000
acagagtgta tcctaatggt ttgttcatta tattacactt tcagtaaaaa 2050
aa 2052

<210> 148
<211> 500
<212> PRT
<213> Homo sapiens

<400> 148

Met	Ala	Leu	Met	Leu	Ser	Leu	Val	Leu	Ser	Leu	Leu	Lys	Leu	Gly	1	5	10	15
Ser	Gly	Gln	Trp	Gln	Val	Phe	Gly	Pro	Asp	Lys	Pro	Val	Gln	Ala	20	25	30	
Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys	35	40	45	
Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe	50	55	60	
Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe	65	70	75	
Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp	80	85	90	
Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr	95	100	105	
Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser	110	115	120	
Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly	125	130	135	
Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile	140	145	150	
Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala	155	160	165	
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg	170	175	180	
Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu	185	190	195	
Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His	200	205	210	
Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp	215	220	225	
Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu				

	230		235		240
Gly Ile Leu Cys	Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys			
	245	250			255
Ile Phe Phe Ser	Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp			
	260	265			270
Trp Arg Arg Lys	His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys			
	275	280			285
His Ala Val Glu	Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys			
	290	295			300
Leu Cys Val Ser	Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro			
	305	310			315
Gln Glu Val Pro	His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val			
	320	325			330
Val Ala Ser Gln	Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val			
	335	340			345
Asp Gly Gly His	Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp			
	350	355			360
Asp Val Asp Arg	Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His			
	365	370			375
Gly Tyr Trp Val	Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr			
	380	385			390
Leu Asn Pro Arg	Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr			
	395	400			405
Lys Ile Gly Val	Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe			
	410	415			420
Phe Asn Ile Asn	Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg			
	425	430			435
Phe Glu Gly Leu	Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn			
	440	445			450
Glu Gln Asn Gly	Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu			
	455	460			465
Ser Glu Lys Glu	Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu			
	470	475			480
Thr Ser Asn Ser	Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu			
	485	490			495
Pro Arg Gly Glu	Met				
	500				

<210> 149

<211> 24

<212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 149
 gcgtggtcca cctctacagg gacg 24

<210> 150
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 150
 ggaactgacc cagtgtgac acc 23

<210> 151
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 151
 gcagatgcc cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
 <211> 2294
 <212> DNA
 <213> Homo sapiens

<400> 152
 gcgatggtgc gcccggtggc ggtggcggcg gcggttgcg aggccttcctt 50
 ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
 aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150
 gcctcgccct gttgtgctgc gccgcccgcg ccgcccgcgt cgcctcagcc 200
 gcctcggcgg ggaatgtcac cggcggcggc ggggccgcgg ggcaggtgga 250
 cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300
 gggcgacggc tcccacggc caggccccga ggaccgggc cccgcgcgc 350
 accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

caccctctt tggcgactg ctggaccctc ttccaccacc tttcaggcgc 450
cgctcggccc ctgcggacc acccctccgg cggcggaacg cacttcgacc 500
acctctcagg cgccgaccag acccgcgccg accacccttt cgaagaccac 550
tggtccggcg ccgaccaccc ctgtagcgac caccgtaccg gcgcccacga 600
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agaccacagg gcagtgtgag tgcggccag gttatcaggg gcttcactgt 800
gaaacctgca aagagggtt ttacctaaat tacactttct ggctctgtca 850
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aagcaacaga ggggtggaact gaagtttatt ttatttttagc aagggaacaa 950
aaaaggctgc tactctcaag gaccatactg gtttaacaa aggaggatga 1000
gggtcataga ttacaaaat attttatata cttttattct cttactttat 1050
atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100
tcttcaaaag cactagagtc gccaatTTTT ctctgggata atttctgtaa 1150
atttcattgg aaaaaattat tgaagaataa atctgctttc tggaagggtc 1200
ttcaggcatg aaacctgcta ggaggtttag aaatgttctt atgtttatta 1250
atataccatt ggagtttgag gaaatttggt gtttggttta tttttctctc 1300
taatcaaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350
ggtaccctaa tttatttaac tagtggttaag tagactggtt ttactctatt 1400
taccagtaca tttttgagac caaaagtaga ttaagcagga attatcttta 1450
aactattatg ttatttgag gtaatttaat ctagtggaat aatgtactgt 1500
tatctaagca tttgccttgt actgcactga aagtaattat tctttgacct 1550
tatgtgaggc acttggtttt ttgtggaccc caagtcaaaa aactgaagag 1600
acagtattaa ataataaaaa aaataatgac aggttatact cagtgttaacc 1650
tggttataac ccaagatctg ctgccactta cgagctgtgt tccttgggca 1700
agtaatttcc tttcactgag cttgtttctt ctcaagggtt ttgtgaagat 1750
taaagaggtt gatatatata aaatgcctag cacatgtcac tcaataaatt 1800
ctgggttggt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

tgttttaaga acttttagct ccttgacaaa gaagtgcttt atacttttagc 1900
 actaaatatt ttaaagtctt tataaatgat attatactgt tatggaatat 1950
 tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000
 ctcacgcctg taatcctagc actttgggag gccaaaggcgg gtggatcact 2050
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 ctactaaaaa tacaacaaa ttagctgggc gtggtggcac acacctgtag 2150
 tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200
 tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250
 agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys	1	5	10	15
Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn	20	25	30	
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro	35	40	45	
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala	50	55	60	
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala	65	70	75	
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro	80	85	90	
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr	95	100	105	
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala	110	115	120	
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro	125	130	135	
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val	140	145	150	
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro	155	160	165	
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro				

	170		175		180
Ala Thr Glu Ala	Pro Ser Ser Pro Pro	Pro Glu Tyr Val Cys Asn			
	185	190			195
Cys Ser Val Val	Gly Ser Leu Asn Val	Asn Arg Cys Asn Gln Thr			
	200	205			210
Thr Gly Gln Cys	Glu Cys Arg Pro Gly	Tyr Gln Gly Leu His Cys			
	215	220			225
Glu Thr Cys Lys	Glu Gly Phe Tyr Leu	Asn Tyr Thr Ser Gly Leu			
	230	235			240
Cys Gln Pro Cys	Asp Cys Ser Pro His	Gly Ala Leu Ser Ile Pro			
	245	250			255

Cys Asn Arg

<210> 154
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 154
 aactgctctg tgggttgaag cctg 24

<210> 155
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 155
 cagtcacatg gctgacagac ccac 24

<210> 156
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-38
 <223> Synthetic construct.

<400> 156
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
 tgcggcgccag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50
 ttctggctttt ggtctcggtg cccagggccc aggccgtgtg gttgggaaga 100
 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtgccctc 150
 ccgggaaaag ggctttgccca tggagaagga catgaagaac gtcgtggggg 200
 tgggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
 cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300
 ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350
 tgctggccac caacttcaga gactatgccca tcattctcac tcagctggag 400
 ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
 agccagccag gagggcatgg ggctcttcac caagtggagc aggagcctgg 500
 gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600
 gggtcctgtg acctcgcca gtgtccaccc acctcgctca gcggctcccg 650
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
 1 5 10 15
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
				95					100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
				110					115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
				125					130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
				140					145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
				155					160					

<210> 159
 <211> 1665
 <212> DNA
 <213> Homo sapiens

<400> 159
 aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50
 gctgctgctg cccctgctct gggggaggga gagggcgga ggacagacaa 100
 gtaaactgct gacgatgcag agttccgtga cggatgcagga aggcctgtgt 150
 gtocatgtgc cctgctcctt ctctacccc tcgcatggct ggatttaccc 200
 tggcccagta gttcatggct actggttccg ggaaggggcc aatacagacc 250
 aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag 300
 actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
 cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400
 gtatggagaa aggaagtata aaatggaatt ataaacatca ccggtctctc 450
 gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
 cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550
 gtgagcaggg gacaccccct atgatctcct ggataggac ctccgtgtcc 600
 cccctggacc cctccaccac ccgctcctcg gtgtcacc tcatcccaca 650
 gcccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
 ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctaccgcct 750
 cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
 cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgccc 850
 tggctctgtc agttgatgca gttgacagca atccccctgc caggctgagc 900
 ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaaccggg 950

ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000
 gcagagctca gaaccctctc ggctctcagc aggtctacct gaacgtctcc 1050
 ctgcagagca aagccacatc aggagtgact caggggggtgg tcggggggagc 1100
 tggagccaca gccctggtct tcctgtcctt ctgcgtcatc ttcgtttag 1150
 tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200
 acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctcagggggcc 1250
 cctgactgaa ccttgggcag aagacagtcc cccagaccag cctccccag 1300
 cttctgcccg ctcctcagtg ggggaaggag agctccagta tgcattccctc 1350
 agcttccaga tggatgaagcc ttgggactcg cggggacagg aggccactga 1400
 caccgagtac tcggagatca agatccacag atgagaaact gcagagactc 1450
 accctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500
 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataaact 1550
 atgaattatg tgcagagtga aaagcacaca ggctttagag tcaaagtatc 1600
 tcaaacctga atccacactg tgccctccct tttatttttt taactaaaag 1650
 acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala
1				5					10					15
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr
				20					25					30
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr
				50					55					60
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala
				65					70					75
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg
				80					85					90
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser
				95					100					105
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg

	110		115		120
Met Glu Lys Gly	Ser Ile Lys Trp Asn	Tyr Lys His His Arg	Leu		
	125	130	135		
Ser Val Asn Val	Thr Ala Leu Thr His	Arg Pro Asn Ile Leu	Ile		
	140	145	150		
Pro Gly Thr Leu	Glu Ser Gly Cys Pro	Gln Asn Leu Thr Cys	Ser		
	155	160	165		
Val Pro Trp Ala	Cys Glu Gln Gly Thr	Pro Pro Met Ile Ser	Trp		
	170	175	180		
Ile Gly Thr Ser	Val Ser Pro Leu Asp	Pro Ser Thr Thr Arg	Ser		
	185	190	195		
Ser Val Leu Thr	Leu Ile Pro Gln Pro	Gln Asp His Gly Thr	Ser		
	200	205	210		
Leu Thr Cys Gln	Val Thr Phe Pro Gly	Ala Ser Val Thr Thr	Asn		
	215	220	225		
Lys Thr Val His	Leu Asn Val Ser Tyr	Pro Pro Gln Asn Leu	Thr		
	230	235	240		
Met Thr Val Phe	Gln Gly Asp Gly Thr	Val Ser Thr Val Leu	Gly		
	245	250	255		
Asn Gly Ser Ser	Leu Ser Leu Pro Glu	Gly Gln Ser Leu Arg	Leu		
	260	265	270		
Val Cys Ala Val	Asp Ala Val Asp Ser	Asn Pro Pro Ala Arg	Leu		
	275	280	285		
Ser Leu Ser Trp	Arg Gly Leu Thr Leu	Cys Pro Ser Gln Pro	Ser		
	290	295	300		
Asn Pro Gly Val	Leu Glu Leu Pro Trp	Val His Leu Arg Asp	Ala		
	305	310	315		
Ala Glu Phe Thr	Cys Arg Ala Gln Asn	Pro Leu Gly Ser Gln	Gln		
	320	325	330		
Val Tyr Leu Asn	Val Ser Leu Gln Ser	Lys Ala Thr Ser Gly	Val		
	335	340	345		
Thr Gln Gly Val	Val Gly Gly Ala Gly	Ala Thr Ala Leu Val	Phe		
	350	355	360		
Leu Ser Phe Cys	Val Ile Phe Val Val	Val Arg Ser Cys Arg	Lys		
	365	370	375		
Lys Ser Ala Arg	Pro Ala Ala Gly Val	Gly Asp Thr Gly Ile	Glu		
	380	385	390		
Asp Ala Asn Ala	Val Arg Gly Ser Ala	Ser Gln Gly Pro Leu	Thr		
	395	400	405		

Glu	Pro	Trp	Ala	Glu	Asp	Ser	Pro	Pro	Asp	Gln	Pro	Pro	Pro	Ala
				410					415					420
Ser	Ala	Arg	Ser	Ser	Val	Gly	Glu	Gly	Glu	Leu	Gln	Tyr	Ala	Ser
				425					430					435
Leu	Ser	Phe	Gln	Met	Val	Lys	Pro	Trp	Asp	Ser	Arg	Gly	Gln	Glu
				440					445					450
Ala	Thr	Asp	Thr	Glu	Tyr	Ser	Glu	Ile	Lys	Ile	His	Arg		
				455					460					

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
 gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50
 accctgtttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100
 cctggaggag gaggatatca cagggaacctg gtacgtgaag gccatggtgg 150
 tcgataagga ctttcoggag gacaggaggc ccaggaaggt gtccccagt 200
 aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcac 250
 gagggaggat cgggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgcccc ggagggacca ctacatcttt tactgcaaag accagcacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
 accgggaggc cctggaagaa ttttaagaaat tgggtgcagcg caagggactc 500
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccg 550
 aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctacc tccagccatg acccttcct 650
 gctccacccc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20										25					30				
Val	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg					
				35					40					45					
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly					
				50					55					60					
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile					
				65					70					75					
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr					
				80					85					90					
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro					
				95					100					105					
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly					
				110					115					120					
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr					
				125					130					135					
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys					
				140					145					150					
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser					
				155					160					165					
Cys	Val	Pro	Glu	His															
				170															

<210> 163
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 163
 ggagatgaag accctgttcc tg 22

<210> 164
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 164
 ggagatgaag accctgttcc tgggtg 26

<210> 165
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct.

<400> 165
gtcctccgga aagtccttat c 21

<210> 166
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 166
gcctagtgtt cggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 167
caggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 168
ctgtccttca ccctggagga ggaggatatc acaggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169

gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcacgagg 50
 cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100
 aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150
 gtagggggag agaccaggat catcaagggg ttcgagtgca agcctcactc 200
 ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtgggg 250
 cgacgctcat cgccccaga tggctcctga cagcagccca ctgcctcaag 300
 ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350
 ctgtgagcag acccggacag ccaactgagtc cttccccac cccggcttca 400
 acaacagcct ccccaacaaa gaccaccgca atgacatcat gctggtgaag 450
 atggcatcgc cagtctccat cacctgggct gtgcgacccc tcacctctc 500
 ctcacgtgt gtcactgtg gcaccagctg cctcatttcc ggctggggca 550
 gcacgtccag cccccagtta cgctgcctc acaccttgcg atgcgccaac 600
 atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650
 cacagacacc atgggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
 gccaggggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750
 attatctcct ggggccagga tccgtgtgcg atcaccgaa agcctggtgt 800
 ctacacgaaa gtctgcaa atgtggactg gatccaggag acgatgaaga 850
 acaattagac tggaccacc caccacagcc catcacctc catttccact 900
 tgggtgtttgg ttctgttca ctctgttaat aagaaaccct aagccaagac 950
 cctctacgaa cattcttgg gcctcctgga ctacaggaga tgctgtcact 1000
 taataatcaa cctgggggtc gaaatcagtg agacctggat tcaaattctg 1050
 ccttgaaata ttgtgactct gggaatgaca acacctggtt tgttctctgt 1100
 tgtatcccca gcccaaaga cagctcctgg ccatatatca aggtttcaat 1150
 aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
 aaaa 1204

<210> 170

<211> 250

<212> PRT

<213> Homo sapiens

<400> 170

Met	Arg	Ile	Leu	Gln	Leu	Ile	Leu	Leu	Ala	Leu	Ala	Thr	Gly	Leu
1				5				10					15	

Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro		20	25	30
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu		35	40	45
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala		50	55	60
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His		65	70	75
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr		80	85	90
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys		95	100	105
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val		110	115	120
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys		125	130	135
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr		140	145	150
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn		155	160	165
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly		170	175	180
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly		185	190	195
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn		200	205	210
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala		215	220	225
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val		230	235	240
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn							245	250	

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 171
ggctgcggga ctggaagtca tcggg 25

<210> 172
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 172
ctccaggcca tgaggattct gcag 24

<210> 173
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 173
cctctgggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 174
tctgtgatgt tgccggggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 175
cgtgtagaca ccaggctttc gggtg 25

<210> 176
<211> 18
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaat atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaagg agacctacta aatgcccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttgtt cttggtgttg ggcaagtc 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450
 tgtgaccaa ggaccacgga gcattgagac atttaaaca atagacatgg 500
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550
 gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600
 tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650
 ctcccaagga atacaatgta taccaacacg atgaactata gcataattgt 700
 atttctactt ttttttttta gctatttact gtactttatg tataaaacaa 750
 agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800
 ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctggt 850
 ttgcaaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
 aaaaaaa 907

<210> 180
 <211> 222
 <212> PRT
 <213> Homo sapiens

<400> 180
 Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
 1 5 10 15
 Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu
 20 25 30
 Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn
 35 40 45
 Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr
 50 55 60
 Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg
 65 70 75
 Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly
 80 85 90
 Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro
 95 100 105
 Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly
 110 115 120
 Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu
 125 130 135
 Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser
 140 145 150

Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu
				155					160					165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys
				170					175					180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu
				185					190					195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser
				200					205					210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu			
				215					220					

<210> 181
 <211> 22
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

 <400> 181
 gtgttctgct ggagccgatg cc 22

 <210> 182
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 182
 gacatggaca atgacagg 18

 <210> 183
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 183
 cctttcagga tgtaggag 18

 <210> 184
 <211> 18
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 184
gatgtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-27
<223> Synthetic construct.

<400> 185
gcatactgat atgacttgct acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 186
tacaagaggg aagaggagtt gcac 24

<210> 187
<211> 52
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-52
<223> Synthetic construct.

<400> 187
gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50
cc 52

<210> 188
<211> 573
<212> DNA
<213> Homo sapiens

<400> 188
cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50
ctctttggag ctgtgactca gaaaacaaaa acttcctgtg ctaagtgcc 100

cccaaatgct tcctgtgtca ataacactca ctgcacctgc aacctatggat 150
 atacttcttg atctgggcag aaactattca cattcccctt ggagacatgt 200
 aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250
 aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
 atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350
 ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaaatcg 400
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500
 ttcttgtttc atttcgcgac tgccctctca gtgtttcctg ggatcccctc 550
 ccaaataaag tacttatatt ctc 573

<210> 189
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 189
 Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
 1 5 10 15
 Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
 20 25 30
 Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
 35 40 45
 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
 50 55 60
 Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
 65 70

<210> 190
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 190
 agggaccatt gcttcttcca ggcc 24

<210> 191
 <211> 24
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 192
cctgtgctaa gtgccccca aatgcttcct gtgtcaataa cactcaactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50
gggtggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100
gacttttgaa gtgaccacc atggggctca gcatcttttt gctcctgtgt 150
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
gctcaactga gcggcagcag gtactgggtg cgcttggggg aacacagcct 350
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
cccatcccgg ctacctgga gcctcgacga gccacgagca cgacctccgg 450
ctgctgcggc tgcgccctgcc cgtccgcgta accagcagcg ttcaaccct 500
gcccctgccc aatgactgtg caaccgctgg caccgagtgc cagctctcag 550
gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600
tgctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
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atgcctgcca ggggtattct gggggcccc tggtgtgtgg gggagtcctt 750
caaggtctgg tgcctgggg gtctgtgggg ccctgtggac aagatggcat 800

ccctggagtc tacacctata tttgcaagta tgtggactgg atccggatga 850
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 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatacttc 950
 ccctagctcc actcttggtg gcctgggaac ttcttgggaac ttttaactcct 1000
 gccagccctt ctaagaccca cgagcggggt gagagaagtg tgcaatagtc 1050
 tggaataaat ataaatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194
 <211> 248
 <212> PRT
 <213> Homo sapiens

<400> 194
 Met Gly Leu Ser Ile Phe Leu Leu Leu Cys Val Leu Gly Leu Ser
 1 5 10 15
 Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg
 20 25 30
 Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu
 35 40 45
 Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala
 50 55 60
 Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His
 65 70 75
 Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly
 80 85 90
 Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His
 95 100 105
 Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val
 110 115 120
 Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr
 125 130 135
 Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His
 140 145 150
 Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser
 155 160 165
 Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile
 170 175 180
 Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala
 185 190 195
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu

	200		205		210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp					
	215		220		225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp					
	230		235		240
Ile Arg Met Ile Met Arg Asn Asn					
	245				

<210> 195
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 195
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 ctggtccctc gccgcgtccg cgaagcctgg agccggcggg agccccgcgc 100
 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcggtc 150
 ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
 caagaccac ctggagatga agaagatgat ctgagagggtg acaggagggg 400
 tcagtacac tatatcctac cgagactttg tgaacatgat gctggggaaa 450
 cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500
 gaggagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
 tgccctgagg accccgcctg gactccccag ccttcccacc ccatacctcc 600
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 ttgggtcccc tccctctctt cttccctcct tccccgctcc ctgtgcagaa 800
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acccaggaca cagccactcg gggccccgct gccccagctg atccccactc 1100
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 tggggtttgg ggggaaaggt cagctcagtg ctgttcacc ttttagggag 1350
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400
 aagtcagcag cactggtaag ccaagactga gaaatacaag gttgcttgtc 1450
 tgaccccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 196
 Met Ser Gly Glu Leu Ser Asn Arg Phe Gln Gly Gly Lys Ala Phe
 1 5 10 15
 Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn
 20 25 30
 Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu
 35 40 45
 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
 50 55 60
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
 65 70 75
 Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys
 80 85 90
 Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr
 95 100 105
 Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu
 110 115 120
 Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro
 125 130 135
 Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro
 140 145 150

<210> 197
 <211> 4842
 <212> DNA
 <213> Homo sapiens

<400> 197

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ggggtcggcg ccgcggtgcg cggccgcctg gcgctggcct tggcgtggc 150
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gctccgctgc cagcgtggac tgccacgggc tgggcctccg cgcggttcct 250
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cccgagcaa gcggcggaac tacgtcttcc agtgcacgga cggctcctcg 4600
tttgtagaag aggtggagag acacttagag tgcggctgcc tcgctgttgc 4650
ctaagcccct gccgcctgc ctgccacctc tcggactcca gcttgatgga 4700
gttgggacag ccatgtggga cccctgggtg attcagcatg aaggaaatga 4750
agctggagag gaaggtaaag aagaagagaa tattaagtat attgtaaaat 4800
aaacaaaaaa tagaacttaa aaaaaaaaaa aaaaaaaaaa aa 4842

<210> 198
<211> 1523
<212> PRT
<213> Homo sapiens

<400> 198
Met Ala Pro Gly Trp Ala Gly Val Gly Ala Ala Val Arg Ala Arg
1 5 10 15
Leu Ala Leu Ala Leu Ala Leu Ala Ser Val Leu Ser Gly Pro Pro
20 25 30
Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val
35 40 45
Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro
50 55 60
Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg
65 70 75
Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu
80 85 90
His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe
95 100 105
Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys
110 115 120
Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu
125 130 135
Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg
140 145 150
Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp
155 160 165

Asn	Asn	His	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu
				170					175					180
Arg	Asp	Leu	Glu	Ile	Leu	Thr	Leu	Asn	Asn	Asn	Asn	Ile	Ser	Arg
				185					190					195
Ile	Leu	Val	Thr	Ser	Phe	Asn	His	Met	Pro	Lys	Ile	Arg	Thr	Leu
				200					205					210
Arg	Leu	His	Ser	Asn	His	Leu	Tyr	Cys	Asp	Cys	His	Leu	Ala	Trp
				215					220					225
Leu	Ser	Asp	Trp	Leu	Arg	Gln	Arg	Arg	Thr	Val	Gly	Gln	Phe	Thr
				230					235					240
Leu	Cys	Met	Ala	Pro	Val	His	Leu	Arg	Gly	Phe	Asn	Val	Ala	Asp
				245					250					255
Val	Gln	Lys	Lys	Glu	Tyr	Val	Cys	Pro	Ala	Pro	His	Ser	Glu	Pro
				260					265					270
Pro	Ser	Cys	Asn	Ala	Asn	Ser	Ile	Ser	Cys	Pro	Ser	Pro	Cys	Thr
				275					280					285
Cys	Ser	Asn	Asn	Ile	Val	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Met	Glu
				290					295					300
Ile	Pro	Ala	Asn	Leu	Pro	Glu	Gly	Ile	Val	Glu	Ile	Arg	Leu	Glu
				305					310					315
Gln	Asn	Ser	Ile	Lys	Ala	Ile	Pro	Ala	Gly	Ala	Phe	Thr	Gln	Tyr
				320					325					330
Lys	Lys	Leu	Lys	Arg	Ile	Asp	Ile	Ser	Lys	Asn	Gln	Ile	Ser	Asp
				335					340					345
Ile	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu	Lys	Ser	Leu	Thr	Ser	Leu
				350					355					360
Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu	Ile	Ala	Lys	Gly	Leu	Phe
				365					370					375
Asp	Gly	Leu	Val	Ser	Leu	Gln	Leu	Leu	Leu	Leu	Asn	Ala	Asn	Lys
				380					385					390
Ile	Asn	Cys	Leu	Arg	Val	Asn	Thr	Phe	Gln	Asp	Leu	Gln	Asn	Leu
				395					400					405
Asn	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Lys	Leu	Gln	Thr	Ile	Ser	Lys
				410					415					420
Gly	Leu	Phe	Ala	Pro	Leu	Gln	Ser	Ile	Gln	Thr	Leu	His	Leu	Ala
				425					430					435
Gln	Asn	Pro	Phe	Val	Cys	Asp	Cys	His	Leu	Lys	Trp	Leu	Ala	Asp
				440					445					450
Tyr	Leu	Gln	Asp	Asn	Pro	Ile	Glu	Thr	Ser	Gly	Ala	Arg	Cys	Ser

Pro	Lys	Asp	Val	Thr	Glu	Leu	Tyr	Leu	Glu	Gly	Asn	His	Leu	Thr	
				755					760					765	
Ala	Val	Pro	Arg	Glu	Leu	Ser	Ala	Leu	Arg	His	Leu	Thr	Leu	Ile	
				770					775					780	
Asp	Leu	Ser	Asn	Asn	Ser	Ile	Ser	Met	Leu	Thr	Asn	Tyr	Thr	Phe	
				785					790					795	
Ser	Asn	Met	Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Ser	Tyr	Asn	Arg	
				800					805					810	
Leu	Arg	Cys	Ile	Pro	Val	His	Ala	Phe	Asn	Gly	Leu	Arg	Ser	Leu	
				815					820					825	
Arg	Val	Leu	Thr	Leu	His	Gly	Asn	Asp	Ile	Ser	Ser	Val	Pro	Glu	
				830					835					840	
Gly	Ser	Phe	Asn	Asp	Leu	Thr	Ser	Leu	Ser	His	Leu	Ala	Leu	Gly	
				845					850					855	
Thr	Asn	Pro	Leu	His	Cys	Asp	Cys	Ser	Leu	Arg	Trp	Leu	Ser	Glu	
				860					865					870	
Trp	Val	Lys	Ala	Gly	Tyr	Lys	Glu	Pro	Gly	Ile	Ala	Arg	Cys	Ser	
				875					880					885	
Ser	Pro	Glu	Pro	Met	Ala	Asp	Arg	Leu	Leu	Leu	Thr	Thr	Pro	Thr	
				890					895					900	
His	Arg	Phe	Gln	Cys	Lys	Gly	Pro	Val	Asp	Ile	Asn	Ile	Val	Ala	
				905					910					915	
Lys	Cys	Asn	Ala	Cys	Leu	Ser	Ser	Pro	Cys	Lys	Asn	Asn	Gly	Thr	
				920					925					930	
Cys	Thr	Gln	Asp	Pro	Val	Glu	Leu	Tyr	Arg	Cys	Ala	Cys	Pro	Tyr	
				935					940					945	
Ser	Tyr	Lys	Gly	Lys	Asp	Cys	Thr	Val	Pro	Ile	Asn	Thr	Cys	Ile	
				950					955					960	
Gln	Asn	Pro	Cys	Gln	His	Gly	Gly	Thr	Cys	His	Leu	Ser	Asp	Ser	
				965					970					975	
His	Lys	Asp	Gly	Phe	Ser	Cys	Ser	Cys	Pro	Leu	Gly	Phe	Glu	Gly	
				980					985					990	
Gln	Arg	Cys	Glu	Ile	Asn	Pro	Asp	Asp	Cys	Glu	Asp	Asn	Asp	Cys	
				995					1000					1005	
Glu	Asn	Asn	Ala	Thr	Cys	Val	Asp	Gly	Ile	Asn	Asn	Tyr	Val	Cys	
				1010					1015					1020	
Ile	Cys	Pro	Pro	Asn	Tyr	Thr	Gly	Glu	Leu	Cys	Asp	Glu	Val	Ile	
				1025					1030					1035	
Asp	His	Cys	Val	Pro	Glu	Leu	Asn	Leu	Cys	Gln	His	Glu	Ala	Lys	

1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly		
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu		
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		
1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
 1340 1345 1350
 Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
 1355 1360 1365
 Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
 1370 1375 1380
 Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
 1385 1390 1395
 Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
 1400 1405 1410
 Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
 1415 1420 1425
 Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
 1430 1435 1440
 Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
 1445 1450 1455
 Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
 1460 1465 1470
 Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
 1475 1480 1485
 Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
 1490 1495 1500
 Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
 1505 1510 1515
 Glu Cys Gly Cys Leu Ala Cys Ser
 1520

<210> 199

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 199

atggagattc ctgccaaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
ttgttggcat tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
gagggcatcg tcgaaatagc cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50
gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100
gaatctgcct ttccagttct gtctccggca ggctttgagg atgaaggctg 150
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250
caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300
agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350
gactatggca tcttcagat caacagcttc gcgtggtgca gacgcggaaa 400
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450
atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500
caaggaatga actattggca aggtggaag aaacattgtg agggcagaga 550
cctgtccgag tggaaaaaag gctgtgaggt ttcttaaact ggaactggac 600
ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650
cctgtgtcat cttgtcccg ttcctccaa tattccttct caaacttgga 700
gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaa 750
gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203
 Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr
 1 5 10 15
 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
 20 25 30
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
 125 130 135
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
 140 145

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 204
 gcaggctttg aggatgaagg ctgc 24

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 205
ctcattggct gcctggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
ctacactcgt tgcaaactgg caaaaatatt ctcgagggt ggcctgg 47

<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
caggccattt gcatccact gtccttgtgt tcggagccag gccacaccgt 50
cctcagcagt gtcattgttt aaaaacgcca agctgaatat atcatgcccc 100
tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagaag 200
gcggaagaag atcctatattt actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300
 gaggaataca ccacagggcat ggcagactgc atcttagtca acagccagtt 350
 cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400
 ctgatgtcct ctatccatct cttaatgtca ccagctttga ctcagttgtt 450
 cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500
 ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcactggaag 550
 ccctagtaca gctgcgtgga agattgacat cccaagattg ggagaggggt 600
 catctgatcg tggcaggtgg ttatgacgag agagtcctgg agaattgtga 650
 acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700
 atgtgacctt cttgaggtct ttctcagaca aacagaaaat ctccctcctc 750
 cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800
 tgtccctctg gaagccatgt acatgcagtg cccagtcatt gctgttaatt 850
 cgggtggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900
 gagcctgacc cgggtgcactt ctcagaagca atagaaaagt tcatccgtga 950
 accttcctta aaagccacca tgggcctggc tggaagagcc agagtgaagg 1000
 aaaaattttc ccctgaagca ttacagaac agctctaccg atatgttacc 1050
 aaactgctgg tataatcaga ttgtttttaa gatctccatt aatgtcattt 1100
 ttatggattg tagaccaggt tttgaaacca aaaaagaaac ctagaatcta 1150
 atgcagaaga gatcttttaa aaaataaact tgagtcttga atgtgagcca 1200
 ctttcctata taccacacct ccctgtccac ttttcagaaa aaccatgtct 1250
 tttatgctat aatcattcca aattttgccg gtgttaagtt acaaattgtg 1300
 tgtcattcca tgttcagcag agtattttta ttatatattt tcgggattat 1350
 tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggttttc 1400
 atagtttaag tgtgtatcat tatcaaagtt gattaatttg gtttcatagt 1450
 ataattgagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500
 tcaactgtcat ctgttaggga atttttgttt gtccctgtctt tgcctggatc 1550
 catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600
 actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaa 1648

<210> 210
 <211> 323

<212> PRT
 <213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	1	5	10	15
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	20	25	30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	35	40	45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	50	55	60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	65	70	75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	80	85	90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	95	100	105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	110	115	120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	125	130	135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	140	145	150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	155	160	165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	170	175	180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	185	190	195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	200	205	210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	215	220	225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	230	235	240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	245	250	255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	260	265	270	

Pro	Asp	Pro	Val	His	Phe	Ser	Glu	Ala	Ile	Glu	Lys	Phe	Ile	Arg
				275					280					285
Glu	Pro	Ser	Leu	Lys	Ala	Thr	Met	Gly	Leu	Ala	Gly	Arg	Ala	Arg
				290					295					300
Val	Lys	Glu	Lys	Phe	Ser	Pro	Glu	Ala	Phe	Thr	Glu	Gln	Leu	Tyr
				305					310					315
Arg	Tyr	Val	Thr	Lys	Leu	Leu	Val							
				320										

<210> 211
 <211> 1554
 <212> DNA
 <213> Homo sapiens

<400> 211
 gactacgacg atccgagacg tggctccctg ggcggcagaa ccatgttgga 50
 cttcgcgacg ttccgccgta ctttcttgct ggcgttggtg ggagccgtgc 100
 tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaa 200
 tttgcatgag ttccctggta atttgcatga gagatatggg cctgtggtct 250
 ccttctgggt tggcaggcgc ctctgtggtta gtttgggcac tgttgatgta 300
 ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaacat 350
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaaa 400
 accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
 agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500
 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
 gttttgctat gaagtctggt acacagatgg taatgggtag tacatttgaa 600
 gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650
 tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
 aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800
 tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
 tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
 tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100
 tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150
 tgggtacttca ggatcctaata acttggccat ctccacacaa gtttgatcca 1200
 gatcgggttg atgatgaatt agtaatgaaa actttttcct cacttggatt 1250
 ctcaggcaca caggagtgtc cagagttgag gtttgcata atggtgacca 1300
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350
 ggacaggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400
 agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaaa atctatgttg 1500
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550
 ttaa 1554

<210> 212
 <211> 462
 <212> PRT
 <213> Homo sapiens

<400> 212
 Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu
 1 5 10 15
 Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala
 20 25 30
 Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu
 35 40 45
 Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn
 50 55 60
 Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg
 65 70 75
 Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His
 80 85 90
 Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys
 95 100 105
 Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn
 110 115 120
 His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu
 125 130 135
 Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu

	140		145		150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr	Gln His Val Pro Leu Ser				
155	160				165
Gln His Met Leu Gly Phe Ala Met Lys	Ser Val Thr Gln Met Val				
170	175				180
Met Gly Ser Thr Phe Glu Asp Asp Gln	Glu Val Ile Arg Phe Gln				
185	190				195
Lys Asn His Gly Thr Val Trp Ser Glu	Ile Gly Lys Gly Phe Leu				
200	205				210
Asp Gly Ser Leu Asp Lys Asn Met Thr	Arg Lys Lys Gln Tyr Glu				
215	220				225
Asp Ala Leu Met Gln Leu Glu Ser Val	Leu Arg Asn Ile Ile Lys				
230	235				240
Glu Arg Lys Gly Arg Asn Phe Ser Gln	His Ile Phe Ile Asp Ser				
245	250				255
Leu Val Gln Gly Asn Leu Asn Asp Gln	Gln Ile Leu Glu Asp Ser				
260	265				270
Met Ile Phe Ser Leu Ala Ser Cys Ile	Ile Thr Ala Lys Leu Cys				
275	280				285
Thr Trp Ala Ile Cys Phe Leu Thr Thr	Ser Glu Glu Val Gln Lys				
290	295				300
Lys Leu Tyr Glu Glu Ile Asn Gln Val	Phe Gly Asn Gly Pro Val				
305	310				315
Thr Pro Glu Lys Ile Glu Gln Leu Arg	Tyr Cys Gln His Val Leu				
320	325				330
Cys Glu Thr Val Arg Thr Ala Lys Leu	Thr Pro Val Ser Ala Gln				
335	340				345
Leu Gln Asp Ile Glu Gly Lys Ile Asp	Arg Phe Ile Ile Pro Arg				
350	355				360
Glu Thr Leu Val Leu Tyr Ala Leu Gly	Val Val Leu Gln Asp Pro				
365	370				375
Asn Thr Trp Pro Ser Pro His Lys Phe	Asp Pro Asp Arg Phe Asp				
380	385				390
Asp Glu Leu Val Met Lys Thr Phe Ser	Ser Leu Gly Phe Ser Gly				
395	400				405
Thr Gln Glu Cys Pro Glu Leu Arg Phe	Ala Tyr Met Val Thr Thr				
410	415				420
Val Leu Leu Ser Val Leu Val Lys Arg	Leu His Leu Leu Ser Val				
425	430				435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
 440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
 455 460

<210> 213
 <211> 759
 <212> DNA
 <213> Homo sapiens

<400> 213
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 tccagcctca gagaccgccg cccttgtccc cgagggccat gggccgggtc 100
 tcagggttg tgccctctcg cttcctgacg ctctggcgc atctggtggt 150
 cgtcatcacc ttattctggt ccggggacag caacatacag gcctgcctgc 200
 ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250
 gcgcgcctct ctgtaccct gggcctcttt gcagtggagc tggccggttt 300
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
 gggctcactg tagtgcaccc gtggccctgt ccttcttcat attcgagcgt 400
 tgggagtgca ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450
 agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
 aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600
 ttccctcggg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700
 tgtttttag tagtaattaag acttatatac agtttttaggg gacaattaa 750
 aaaaaaaaa 759

<210> 214
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 214
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
 1 5 10 15
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
 20 25 30
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
 35 40 45

Tyr	Asp	Lys	Gln	Asp	Ile	Gln	Leu	Val	Ala	Ala	Leu	Ser	Val	Thr	
				50					55					60	
Leu	Gly	Leu	Phe	Ala	Val	Glu	Leu	Ala	Gly	Phe	Leu	Ser	Gly	Val	
				65					70					75	
Ser	Met	Phe	Asn	Ser	Thr	Gln	Ser	Leu	Ile	Ser	Ile	Gly	Ala	His	
				80					85					90	
Cys	Ser	Ala	Ser	Val	Ala	Leu	Ser	Phe	Phe	Ile	Phe	Glu	Arg	Trp	
				95					100					105	
Glu	Cys	Thr	Thr	Tyr	Trp	Tyr	Ile	Phe	Val	Phe	Cys	Ser	Ala	Leu	
				110					115					120	
Pro	Ala	Val	Thr	Glu	Met	Ala	Leu	Phe	Val	Thr	Val	Phe	Gly	Leu	
				125					130					135	
Lys	Lys	Lys	Pro	Phe											
				140											

<210> 215
 <211> 697
 <212> DNA
 <213> Homo sapiens

<400> 215
 tcccggaccc tgccgccctg ccactatgtc ccgccgtct atgctgcttg 50
 cctgggctct cccagcctc cttcgactcg gagcggctca ggagacagaa 100
 gaccggcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150
 ggcacagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200
 tatgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
 caggcccga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
 cgtgggctac aacttctga ttggagaaga cgggctcgta tacgagggcc 350
 gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
 tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
 ccaggccatc cgggcagccc aggtctact ggcctgcggg gtggctcagg 500
 gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550
 aactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
 ctaccgtcc ccctgaggcc ctgctgatcc gcacccatt cctccctcc 650
 catggcaaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216
 <211> 196
 <212> PRT

<213> Homo sapiens

<400> 216

Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu
1 5 10 15
Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys
20 25 30
Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
35 40 45
Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
50 55 60
His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
65 70 75
Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
80 85 90
Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
95 100 105
Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
110 115 120
Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr
125 130 135
Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly
140 145 150
Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr
155 160 165
Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly
170 175 180
Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser
185 190 195
Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

ctgggacccc gaaaagagaa ggggagagcg aggggacgag agcggaggag 50
gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc 100
tctatctggt catctgtggc caggatgatg gtcctcccg ctcagaggac 150
cctgagcgtg atgaaccaga gggccagccc cggccccggg tgcctcggaa 200

gcgggggccac atctcaccta agtcccggccc catggccaat tccactotcc 250
 taggggctgct ggccccgcct ggggaggcctt ggggcattct tgggcagccc 300
 cccaaccgcc cgaaccacag cccccaccc tcagccaagg tgaagaaaat 350
 ctttggtggtg ggcgacttct actccaacat caagacggtg gccctgaacc 400
 tgctcgtcac agggaagatt gtggaccatg gcaatgggac cttcagcgtc 450
 cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500
 gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550
 aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
 gaacgggggcc gccggacctc gctttgcacc cacgacccag ccaagatctg 650
 ctcccagac cacgctcaga gctcagccac ctggagctgc toccagccct 700
 tcaaagtcgt ctgtgtctac atcgcccttct acagcacgga ctatcggtg 750
 gtccagaagg tgtgccaga ttacaactac catagtata cccctacta 800
 cccatctggg tgaccggggg caggccacag aggccaggcc agggctggaa 850
 ggacaggcct gcccatgcag gagaccatct ggacaccggg cagggaaggg 900
 gttgggcctc aggcaggag ggggggtggag acgaggagat gccaagtggg 950
 gccagggcc agtctcaagt ggagagaaa gggtoccaag tgctgggtccc 1000
 aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagtg 1050
 ggctctctgt gcagcctcac agggctttgc cacggagcca cagagagatg 1100
 ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150
 gtcattggag gaagctaagc ccttggttct tgccatcctg aggaaagata 1200
 gcaacaggga gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250
 atggatggct gagagggtt cctaggagcc agtcagcagg gtgggggtggg 1300
 gccagaggag ctctccagcc ctgcctagt ggcgccctga gcccttgtc 1350
 gtgtgctgag catggcatga ggctgaagt gcaaccctgg ggtctttgat 1400
 gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaaa 1450
 ttccctcttc tgccagtact ccccctgtac caccattgc tgatggcaca 1500
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 ctctctggg agcatccatg tcccggagag gggtoctca acagtcagcc 1650

tcacctgtca gaccgggggtt ctcccggtac tggatggcgc cgccctctca 1700
gcagcgggca cgggtggggc ggggcccggc cgcagagcat gtgctggatc 1750
tgttctgtgt gtctgtctgt ggggtggggg aggggagggg agtcttgtga 1800
aaccgtgat tgcgtacttt tgtgtgaaga atcgtgttct tggagcagga 1850
aataaagctt gccccggggc a 1871

<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

Met	Gln	Leu	Thr	Arg	Cys	Cys	Phe	Val	Phe	Leu	Val	Gln	Gly	Ser	1	5	10	15
Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser	20	25	30	
Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg	35	40	45	
Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	50	55	60	
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	65	70	75	
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	80	85	90	
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	95	100	105	
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	110	115	120	
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	125	130	135	
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	140	145	150	
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	155	160	165	
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	170	175	180	
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	185	190	195	
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	200	205	210	

Ser	Cys	Ser	Gln	Pro	Phe	Lys	Val	Val	Cys	Val	Tyr	Ile	Ala	Phe
				215					220					225
Tyr	Ser	Thr	Asp	Tyr	Arg	Leu	Val	Gln	Lys	Val	Cys	Pro	Asp	Tyr
				230					235					240
Asn	Tyr	His	Ser	Asp	Thr	Pro	Tyr	Tyr	Pro	Ser	Gly			
				245					250					

<210> 219
 <211> 2065
 <212> DNA
 <213> Homo sapiens

<400> 219
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 gcagggggccc caggcagggc tgattcttgg gcggaggaga gtagggtaaa 100
 gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150
 agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200
 gcgccgccgc cgccgtcgct cctgcagcgc tgctgaccta gccgctagca 250
 tcttcccagag caccgggatc ccggggtagg aggcgacgcg ggcgagcacc 300
 agcgccagcc ggctgcggct gccacacagg ctacccatgg gctccgggcg 350
 ccgggcgctg tccgcggtgc cgccgtgct gctggtcctc acgctgccgg 400
 ggctgcccgt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450
 aagtgtctgg tgggtgtgca ctogaaccog gccacggact ccaagggctc 500
 ctcttcctcc ccgctgggga tatcggtccg ggccggccaac tccaaggctc 550
 ccttctcggc ggtgcgggag accaaccacg agccatccga gatgagcaac 600
 aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650
 tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700
 tcagttttca cgtgattaaa gtctaccaga gccaaactat ccagggttaac 750
 ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaga 800
 tgttactcgt gaagctgcc acaatggtgt cctgctctac ctagataaag 850
 aggataaggt ttacctaaaa ctggagaaaag gtaatttggt tggaggctgg 900
 cagtattcca cgttttctgg ctttctggtg ttccccctat aggattcaat 950
 ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000
 gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050
 ggtggatatg gattctaagg attctagcct gtctgaacca atacaaaatt 1100

tcacagatta tttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150
 aagcagataa tacctatgct taaatgtaac agtcaaaagc tgtctgcaag 1200
 acttattctg aatttcattt cctgggatta ctgaattagt tacagatgtg 1250
 gaattttatt tgttttagttt taaaagactg gcaaccaggt ctaaggatta 1300
 gaaaactcta aagttctgac ttcaatcaac ggtagtgtg atactgccaa 1350
 agaactgtat actgtgttaa tatattgatt atatttgttt ttattccttt 1400
 ggaattagtt tgtttggttc ttgtaaaaaa cttggatttt ttttttcagt 1450
 aactgggtatt atgttttctc ttaaaataag gtaatgaatg gcttgccac 1500
 aaatttacct tgactacgat atcatcgaca tgacttctct caaaaaaaaa 1550
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 ccaagttata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650
 aaagttgctt acccaaaatc taagtgtca atccctgagc ctcagcaaaa 1700
 cagctcccct ccgagggaaa tcttatactt tattgtctca ctttaattaa 1750
 aatgattgat aataaccact ttattaaaaa cctaaggttt tttttttttc 1800
 cgtagacatg accactttat taactgggtg tgggatgctg ttgtttctaa 1850
 ttataacctat ttttcaaggc ttctgttgta ttggaagtat catctggttt 1900
 tgecttaact ctttaaattg tatatattta tctgttttagc taatattaa 1950
 ttcaaataatc ccatatctaa atttagtgca atatcttgtc ttttgtatag 2000
 gtcatatgaa ttcataaaat tatttatgtc tgttatagaa taaagattaa 2050
 tatatgttaa aaaaa 2065

<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

Met	Gly	Ser	Gly	Arg	Arg	Ala	Leu	Ser	Ala	Val	Pro	Ala	Val	Leu
1				5				10						15

Leu	Val	Leu	Thr	Leu	Pro	Gly	Leu	Pro	Val	Trp	Ala	Gln	Asn	Asp
				20				25						30

Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp
				35				40						45

Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu
				50				55						60

Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	
				65					70					75	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	
				80					85					90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	
				95					100					105	
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	
				110					115					120	
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	
				125					130					135	
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	
				140					145					150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	
				155					160					165	
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	
				170					175					180	
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	
				185					190					195	
Phe	Leu	Val	Phe	Pro	Leu										
				200											

<210> 221
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 221
 acggctcacc atgggctccg 20

<210> 222
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 222
 aggaagagga gcccttgag tccg 24

<210> 223
 <211> 40

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
cgtgctggag ggcaagtgtc tgggtggtgtg cgactcgaac 40

<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
cggtggccat gactgcggcc gtgttcttcg gctgcgcctt cattgccttc 50
gggcctgcgc tcgcccttta tgtcttcacc atcgccatcg agccgttgcg 100
tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250
tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300
gtgaagggtt gaagagtata aaccaggtg agacagcacc ctctatgoga 350
ctgctggcct atgtttcttg cttgggcttt ggaatcatga gtggagtatt 400
ttcctttgtg aataccctat ctgactcctt ggggccaggc acagtgggca 450
ttcatggaga ttctcctcaa ttcttccttt attcagcttt catgacgctg 500
gtcattatct tgctgcatgt attctggggc attgtatitt ttgatggctg 550
tgagaagaaa aagtggggca tcctccttat cgttctcctg acccacctgc 600
tgggtgtcagc ccagaccttc ataagttctt attatggaat aaacctggcg 650
tcagcattta taatcctggg gctcatgggc acctgggcat tcttagctgc 700
gggaggcagc tgccgaagcc tgaaactctg cctgctctgc caagacaaga 750
actttcttct ttacaaccag cgctccagat aacctcaggg aaccagcact 800
tcccaaaccg cagactacat ctttagagga agcacaactg tgccctttttc 850
tgaaaatccc tttttctggt ggaattgaga aagaaataaa actatgcaga 900
ta 902

<210> 225
<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	Ala	Phe	Gly	
1				5					10					15	
Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu	
				20					25					30	
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	
				35					40					45	
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	
				50					55					60	
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	
				65					70					75	
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	
				80					85					90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	
				95					100					105	
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	
				110					115					120	
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	
				125					130					135	
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	
				140					145					150	
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	
				155					160					165	
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	
				170					175					180	
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	
				185					190					195	
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	
				200					205					210	
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	
				215					220					225	
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	
				230					235					240	
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg	
				245					250					255	

Ser Arg

<210> 226

<211> 3939
<212> DNA
<213> Homo sapiens

<400> 226
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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

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Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser	35	40	45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn	50	55	60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln	65	70	75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val	80	85	90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg	95	100	105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro	110	115	120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser	125	130	135
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg	140	145	150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn	155	160	165
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu	170	175	180
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe	185	190	195
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr	200	205	210
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met	215	220	225
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser	230	235	240
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala	245	250	255
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro	260	265	270
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser	275	280	285
Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys	290	295	300
Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala	305	310	315
Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala			

	320		325		330
Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala	335		340		345
Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly	350		355		360
Ser Phe Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser	365		370		375
Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg Ser Phe	380		385		390
Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val	395		400		405
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys	410		415		420
Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala	425		430		435
Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe	440		445		450
Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val	455		460		465
Gln Leu Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn	470		475		480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly	485		490		495
Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile	500		505		510
Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile	515		520		525
Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu Glu	530		535		540
Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr	545		550		555
Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys	560		565		570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met	575		580		585
Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro	590		595		600
Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile	605		610		615

Val	Ile	Phe	Phe	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn	
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Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr	
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Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu	
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Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp	
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Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val	
				680					685					690	
Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr	
				695					700					705	
Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala	
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Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile	
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Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe	
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Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser	
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Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp	
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His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser	
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Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln	
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Arg	Asp	Lys	Ile	Tyr	Val	Phe									
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<210> 228

<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

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<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

Met	Val	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Cys	Val	Ser	Val	Pro	Gln
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	20	25	30
Glu Asn Tyr Gly Gly Asn Phe Pro Leu Tyr Leu Thr Lys Leu Pro	35	40	45
Leu Pro Arg Glu Gly Ala Glu Gly Gln Ile Val Leu Ser Gly Asp	50	55	60
Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala Met Asp Pro Asp Ser	65	70	75
Gly Phe Leu Leu Val Thr Arg Ala Leu Asp Arg Glu Glu Gln Ala	80	85	90
Glu Tyr Gln Leu Gln Val Thr Leu Glu Met Gln Asp Gly His Val	95	100	105
Leu Trp Gly Pro Gln Pro Val Leu Val His Val Lys Asp Glu Asn	110	115	120
Asp Gln Val Pro His Phe Ser Gln Ala Ile Tyr Arg Ala Arg Leu	125	130	135
Ser Arg Gly Thr Arg Pro Gly Ile Pro Phe Leu Phe Leu Glu Ala	140	145	150
Ser Asp Arg Asp Glu Pro Gly Thr Ala Asn Ser Asp Leu Arg Phe	155	160	165
His Ile Leu Ser Gln Ala Pro Ala Gln Pro Ser Pro Asp Met Phe	170	175	180
Gln Leu Glu Pro Arg Leu Gly Ala Leu Ala Leu Ser Pro Lys Gly	185	190	195
Ser Thr Ser Leu Asp His Ala Leu Glu Arg Thr Tyr Gln Leu Leu	200	205	210
Val Gln Val Lys Asp Met Gly Asp Gln Ala Ser Gly His Gln Ala	215	220	225
Thr Ala Thr Val Glu Val Ser Ile Ile Glu Ser Thr Trp Val Ser	230	235	240
Leu Glu Pro Ile His Leu Ala Glu Asn Leu Lys Val Leu Tyr Pro	245	250	255
His His Met Ala Gln Val His Trp Ser Gly Gly Asp Val His Tyr	260	265	270
His Leu Glu Ser His Pro Pro Gly Pro Phe Glu Val Asn Ala Glu	275	280	285
Gly Asn Leu Tyr Val Thr Arg Glu Leu Asp Arg Glu Ala Gln Ala	290	295	300
Glu Tyr Leu Leu Gln Val Arg Ala Gln Asn Ser His Gly Glu Asp	305	310	315

Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn	320	325	330
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile	335	340	345
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala	350	355	360
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr	365	370	375
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala	380	385	390
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu	395	400	405
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met	410	415	420
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val	425	430	435
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile	440	445	450
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro	455	460	465
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu	470	475	480
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr	485	490	495
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val	500	505	510
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser	515	520	525
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly	530	535	540
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val	545	550	555
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu	560	565	570
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr	575	580	585
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu	590	595	600
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly			

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Glu Val His Thr	Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly	Asp		
	620	625	630		
Thr Tyr Thr Val	Leu Val Glu Ala Gln	Asp Thr Ala Leu Thr	Leu		
	635	640	645		
Ala Pro Val Pro	Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp	His		
	650	655	660		
Gly Leu Ile Val	Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala	Ser		
	665	670	675		
Gly His Gly Pro	Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr	Val		
	680	685	690		
Gln Arg Asp Trp	Arg Leu Gln Thr Leu	Asn Gly Ser His Ala	Tyr		
	695	700	705		
Leu Thr Leu Ala	Leu His Trp Val Glu	Pro Arg Glu His Ile	Ile		
	710	715	720		
Pro Val Val Val	Ser His Asn Ala Gln	Met Trp Gln Leu Leu	Val		
	725	730	735		
Arg Val Ile Val	Cys Arg Cys Asn Val	Glu Gly Gln Cys Met	Arg		
	740	745	750		
Lys Val Gly Arg	Met Lys Gly Met Pro	Thr Lys Leu Ser Ala	Val		
	755	760	765		
Gly Ile Leu Val	Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu	Ile		
	770	775	780		
Leu Ile Phe Thr	His Trp Thr Met Ser	Arg Lys Lys Asp Pro	Asp		
	785	790	795		
Gln Pro Ala Asp	Ser Val Pro Leu Lys	Ala Thr Val			
	800	805			

<210> 230
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 230
 cgccttaccg cgcagcccga agattcacta tgggtgaaaat cgccttcaat 50

<210> 231
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
<221> Artificial Sequence
<222> full
<223> Synthetic oligonucleotide probe

<400> 231
cctgagctgt aaccccactc cagg 24

<210> 232
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 232
agagtctgtc ccagctatct tgt 23

<210> 233
<211> 2786
<212> DNA
<213> Homo sapiens

<400> 233
ccggggacat gaggtggata ctgttcattg gggcccttat tgggtccagc 50
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cagaaatgga gacgagatca gcaattgag tcaactagtg aattcaaaca 150
acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200
gatgtcctgg tcccatctgt cagtctgcag gcattttaa ccttctgtgag 250
atcccagggc ttagagtacg cagtgacaat tgaggacctg caggcccttt 300
tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350
agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400
cgagatggac aacattgccg cagactttcc tgacctggcg aggaggggtga 450
agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500
actgggaaag gcgtgaggcg gccggccgtt tggctgaatg caggcatcca 550
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ggaaaggag ccagcgacaa cccttgctcc gaagtgtacc atggaccca 850

cgccaattcg gaagtggagg tgaatcagt gtagatttc atccaaaaac 900
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 ccaataaata ttcaatgtga aaaaaaaaaa aaaaaa 2786

<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

Met	Arg	Trp	Ile	Leu	Phe	Ile	Gly	Ala	Leu	Ile	Gly	Ser	Ser	Ile	1	5	10	15
Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn	20	25	30	
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn	35	40	45	
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe	50	55	60	
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala	65	70	75	
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr	80	85	90	
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met	95	100	105	
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr	110	115	120	
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn	125	130	135	
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly	140	145	150	
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr	155	160	165	

Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile	170	175	180
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala	185	190	195
Arg	Lys	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr	Ser	200	205	210
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn	Pro	215	220	225
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys	230	235	240
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp	Pro	245	250	255
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser	Asp	260	265	270
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser	Glu	275	280	285
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly	Asn	290	295	300
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu	Met	305	310	315
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu	320	325	330
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val	335	340	345
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val	Tyr	350	355	360
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile	365	370	375
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	380	385	390
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr	395	400	405
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn	Leu	410	415	420

Tyr

<210> 235
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<400> 235

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tggtccaaaa tggcatctta ctttatgga gtactctttg ctggtggcct 100
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cccgcccttc ctccacaaag agcaccctg cctcacaggt gtattccctc 200
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tgctctccct tggggcccac tcagtcacca agaccagat tctccagggc 350
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agaagacca agggaagggt gtagacataa tccaaggcct tgaccttctg 650
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 ggatgttgct gggttaccat atttccattc cttggggctc ccaggaatgg 1600
 aaatacgcca acccagggtta ggcacctcta ttgcagaatt acaataacac 1650
 attcaataaaa actaaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 236
 Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys
 1 5 10 15
 Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr
 20 25 30
 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr
 35 40 45
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
 50 55 60
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val
 65 70 75
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr
 80 85 90
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
 95 100 105
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
 110 115 120
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
 125 130 135
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
 140 145 150
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
 155 160 165
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
 170 175 180
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
 185 190 195
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala

200	205	210
Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe		
215	220	225
Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met		
230	235	240
His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn		
245	250	255
Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe		
260	265	270
Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala		
275	280	285
Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys		
290	295	300
Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser		
305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala		
320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser		
335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser		
350	355	360
Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile		
365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn		
380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile		
395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser		
410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
ctttgctggtt ggcctctgtg ctccaacca tgcaaggaca gggcagg 47

<210> 239
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 239
tgactcgggg tctccaaaac cagc 24

<210> 240
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 240
ggtataggcg gaaggcaaag tcgg 24

<210> 241
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
ggctgaccgt gctacattgc ctggaggaag cctaaggaaac ccaggcatcc 50

agctgcccac gcctgagtc aagattcttc ccaggaacac aaacgtagga 100
 gaccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150
 ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200
 ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250
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 gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243
 <211> 596
 <212> PRT
 <213> Homo sapiens

<400> 243
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 Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser
 20 25 30
 Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala
 35 40 45
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala
 50 55 60
 Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val
 65 70 75

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala	
				80					85					90	
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala	
				95					100					105	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				110					115					120	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	
				125					130					135	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				140					145					150	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				155					160					165	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				170					175					180	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				185					190					195	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				200					205					210	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				215					220					225	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				230					235					240	
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala	
				245					250					255	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				260					265					270	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				275					280					285	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				290					295					300	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				305					310					315	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	
				320					325					330	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	
				335					340					345	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	
				350					355					360	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala	

gaagcaccag ctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic sequence.

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 246

ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50

ttcccgaacct tcccagcaat atgcatcttg cacgtctggt cggctcctgc 100

tccctccttc tgctactggg ggccctgtct ggatgggagg ccagcgatga 150

ccccattgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200

agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250

gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300

ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350

tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaag 400

gaagcagaga agcttgGCCa tggggTcaac aacgctgctg gacaggccgg 450

gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500

ctgggaagga agcagagaaa cttggccaag gggTcaacca tgctgctgac 550

caggctggaa aggaagtgga gaagcttggc caaggtgccc accatgctgc 600

tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650
 ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700
 tccagccatc aaggaggggc cacaaccacg ccgtagcct ctggggcctc 750
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 acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850
 gttgtcacat cagctgacat gacctggagg ggttgggggt gggggacagg 900
 tttctgaaat ccctgaaggg ggttgtactg ggatttgtga ataaacttga 950
 tacacca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	1	5	10	15
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	20	25	30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	35	40	45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	50	55	60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	65	70	75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	80	85	90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	95	100	105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	110	115	120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	125	130	135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	140	145	150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	155	160	165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	170	175	180	

Gly	Lys	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser
				185					190					195
Lys	Glu	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser
				200					205					210
Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly
				215					220					225
Ala	Ser	Val	Asn	Thr	Pro	Phe	Ile	Asn	Leu	Pro	Ala	Leu	Trp	Arg
				230					235					240
Ser	Val	Ala	Asn	Ile	Met	Pro								
				245										

<210> 249

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 249

caatatgcat cttgcacgtc tgg 23

<210> 250

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 250

aagcttctct gcttcctttc ctgc 24

<210> 251

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 251

tgacccatt gagaaggatca ttgaaggat caaccgagg ctg 43

<210> 252

<211> 3781

<212> DNA

<213> Homo sapiens

<400> 252

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tgaccctgac tcaactccagg tccggaggcg ggggcccccg gggcgactcg 150
ggggcggaacc gcggggcgga gctgccgcc gtgagtccgg ccgagccacc 200
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tcagcccat gtgtacctac atcaacatgg agaacttcac cctggcaagg 750
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 gtttttatac attttttaat aagatgcact ttatgtcatt ttttaataaa 3750
 gtctgaagaa ttactgttta aaaaaaaaaa a 3781

<210> 253
 <211> 837
 <212> PRT
 <213> Homo sapiens

<400> 253
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 Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu Leu
 20 25 30
 Leu Leu Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser
 35 40 45
 Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu
 50 55 60
 Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu
 65 70 75
 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

80					85					90				
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr
				95					100					105
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys
				110					115					120
Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile
				125					130					135
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly
				140					145					150
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn
				155					160					165
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp
				170					175					180
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala
				185					190					195
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe
				200					205					210
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro
				215					220					225
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe
				230					235					240
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly
				245					250					255
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu
				260					265					270
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile
				275					280					285
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp
				290					295					300
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp
				305					310					315
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro
				320					325					330
Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr
				335					340					345
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val
				350					355					360
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys
				365					370					375

Glu	Val	Asn	Arg	Glu	Thr	Gln	Gln	Trp	Tyr	Thr	Val	Thr	His	Pro	380	385	390
Val	Pro	Thr	Pro	Arg	Pro	Gly	Ala	Cys	Ile	Thr	Asn	Ser	Ala	Arg	395	400	405
Glu	Arg	Lys	Ile	Asn	Ser	Ser	Leu	Gln	Leu	Pro	Asp	Arg	Val	Leu	410	415	420
Asn	Phe	Leu	Lys	Asp	His	Phe	Leu	Met	Asp	Gly	Gln	Val	Arg	Ser	425	430	435
Arg	Met	Leu	Leu	Leu	Gln	Pro	Gln	Ala	Arg	Tyr	Gln	Arg	Val	Ala	440	445	450
Val	His	Arg	Val	Pro	Gly	Leu	His	His	Thr	Tyr	Asp	Val	Leu	Phe	455	460	465
Leu	Gly	Thr	Gly	Asp	Gly	Arg	Leu	His	Lys	Ala	Val	Ser	Val	Gly	470	475	480
Pro	Arg	Val	His	Ile	Ile	Glu	Glu	Leu	Gln	Ile	Phe	Ser	Ser	Gly	485	490	495
Gln	Pro	Val	Gln	Asn	Leu	Leu	Leu	Asp	Thr	His	Arg	Gly	Leu	Leu	500	505	510
Tyr	Ala	Ala	Ser	His	Ser	Gly	Val	Val	Gln	Val	Pro	Met	Ala	Asn	515	520	525
Cys	Ser	Leu	Tyr	Arg	Ser	Cys	Gly	Asp	Cys	Leu	Leu	Ala	Arg	Asp	530	535	540
Pro	Tyr	Cys	Ala	Trp	Ser	Gly	Ser	Ser	Cys	Lys	His	Val	Ser	Leu	545	550	555
Tyr	Gln	Pro	Gln	Leu	Ala	Thr	Arg	Pro	Trp	Ile	Gln	Asp	Ile	Glu	560	565	570
Gly	Ala	Ser	Ala	Lys	Asp	Leu	Cys	Ser	Ala	Ser	Ser	Val	Val	Ser	575	580	585
Pro	Ser	Phe	Val	Pro	Thr	Gly	Glu	Lys	Pro	Cys	Glu	Gln	Val	Gln	590	595	600
Phe	Gln	Pro	Asn	Thr	Val	Asn	Thr	Leu	Ala	Cys	Pro	Leu	Leu	Ser	605	610	615
Asn	Leu	Ala	Thr	Arg	Leu	Trp	Leu	Arg	Asn	Gly	Ala	Pro	Val	Asn	620	625	630
Ala	Ser	Ala	Ser	Cys	His	Val	Leu	Pro	Thr	Gly	Asp	Leu	Leu	Leu	635	640	645
Val	Gly	Thr	Gln	Gln	Leu	Gly	Glu	Phe	Gln	Cys	Trp	Ser	Leu	Glu	650	655	660
Glu	Gly	Phe	Gln	Gln	Leu	Val	Ala	Ser	Tyr	Cys	Pro	Glu	Val	Val			

	665		670		675
Glu Asp Gly Val	Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val	Pro		
	680		685		690
Val Ile Ile Ser	Thr Ser Arg Val Ser	Ala Pro Ala Gly Gly	Lys		
	695		700		705
Ala Ser Trp Gly	Ala Asp Arg Ser Tyr	Trp Lys Glu Phe Leu	Val		
	710		715		720
Met Cys Thr Leu	Phe Val Leu Ala Val	Leu Leu Pro Val Leu	Phe		
	725		730		735
Leu Leu Tyr Arg	His Arg Asn Ser Met	Lys Val Phe Leu Lys	Gln		
	740		745		750
Gly Glu Cys Ala	Ser Val His Pro Lys	Thr Cys Pro Val Val	Leu		
	755		760		765
Pro Pro Glu Thr	Arg Pro Leu Asn Gly	Leu Gly Pro Pro Ser	Thr		
	770		775		780
Pro Leu Asp His	Arg Gly Tyr Gln Ser	Leu Ser Asp Ser Pro	Pro		
	785		790		795
Gly Ala Arg Val	Phe Thr Glu Ser Glu	Lys Arg Pro Leu Ser	Ile		
	800		805		810
Gln Asp Ser Phe	Val Glu Val Ser Pro	Val Cys Pro Arg Pro	Arg		
	815		820		825
Val Arg Leu Gly	Ser Glu Ile Arg Asp	Ser Val Val			
	830		835		

<210> 254
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 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 254
 agcccggtgca gaatctgctc ctgg 24

<210> 255
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 255
tgaagccagg gcagcgtcct ctgg 24

<210> 256
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 256
gtacaggctg cagttggc 18

<210> 257
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 257
agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 258
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<210> 259
<211> 4563
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 3635
<223> unknown base

<400> 259
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agggcgggac gggagcccgg actcgtctgc cgccgccgtc gtcgccgtcg 150

tgccggcccc gcgtccccgc gcgcgagcgg gaggagccgc cgccacctcg 200
 cgccccgagcc gccgctagcg cgcgccgggc atggtcccct cttaaaggcg 250
 caggccgcgg cggcgggggc ggggtgtgcgg aacaaagcgc cggcgcgggg 300
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 gcttcccagg ccggcggggc gcgcggcgat gcgcgcgggg cgcagctctg 700
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 ccgcaagata tccgagctcc gccatcgcac aatacagctg caccgcgaaa 1500
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 ggggtgaaccc catgtatggg gctgagtaca tcctggacct gctgcttctg 1850
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<210> 260
 <211> 802
 <212> PRT
 <213> Homo sapiens

<400> 260
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 Leu Val Leu Gly Phe Val Leu Ala Ser Arg Leu Val Leu Pro Arg
 20 25 30
 Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro
 35 40 45
 Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly
 50 55 60
 Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser
 65 70 75
 Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly
 80 85 90
 Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala
 95 100 105
 Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe
 110 115 120
 Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
 125 130 135
 Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
 140 145 150
 Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu
 155 160 165
 Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg
 170 175 180
 Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe
 185 190 195
 Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
 200 205 210
 Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val
 215 220 225
 Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
 230 235 240

Lys Cys Leu Arg	Glu Met Tyr Thr Thr	His Glu Asp Val Glu Val	245	250	255
Gly Arg Cys Val	Arg Arg Phe Ala Gly Val	Gln Cys Val Trp Ser	260	265	270
Tyr Glu Met Arg	Gln Leu Phe Tyr Glu Asn	Tyr Glu Gln Asn Lys	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn Ser	Lys Ile His Gln Ala	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro Pro	Tyr Gln Tyr Arg Leu	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile Ser	Glu Leu Arg His Arg	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val Leu	Met Ser Lys Tyr Ser	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu Gln	Leu Gly Ile Pro Pro	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln Arg	Glu Glu Ile Leu Glu	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu Tyr	Ser Ala Val Asp Gly	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser Ala	Gln Arg Glu Ala Leu	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu Met	Ile Asn Ala Asn Ala	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe Lys	Glu Ile Gln Tyr Gly	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly Ala	Glu Tyr Ile Leu Asp	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys Gly	Lys Lys Met Thr Val	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln Gln	Thr Phe Ser Lys Ile	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp Ala	Gln Glu Leu Ala Lys	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu Ser	Phe Leu Ser Asn Ser	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu Pro	Gly Ser Lys Ser Glu	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile Asn	Ile Leu Ile Pro Leu			

530					535					540				
Ser	Gly	Arg	Phe	Asp	Met	Phe	Val	Arg	Phe	Met	Gly	Asn	Phe	Glu
				545					550					555
Lys	Thr	Cys	Leu	Ile	Pro	Asn	Gln	Asn	Val	Lys	Leu	Val	Val	Leu
				560					565					570
Leu	Phe	Asn	Ser	Asp	Ser	Asn	Pro	Asp	Lys	Ala	Lys	Gln	Val	Glu
				575					580					585
Leu	Met	Arg	Asp	Tyr	Arg	Ile	Lys	Tyr	Pro	Lys	Ala	Asp	Met	Gln
				590					595					600
Ile	Leu	Pro	Val	Ser	Gly	Glu	Phe	Ser	Arg	Ala	Leu	Ala	Leu	Glu
				605					610					615
Val	Gly	Ser	Ser	Gln	Phe	Asn	Asn	Glu	Ser	Leu	Leu	Phe	Phe	Cys
				620					625					630
Asp	Val	Asp	Leu	Val	Phe	Thr	Thr	Glu	Phe	Leu	Gln	Arg	Cys	Arg
				635					640					645
Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile	Tyr	Phe	Pro	Ile	Ile	Phe
				650					655					660
Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys	Val	Pro	Ser
				665					670					675
Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys	Thr	Gly	Phe	Trp	Arg	Asn
				680					685					690
Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg
				695					700					705
Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp
				710					715					720
Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe
				725					730					735
Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe
				740					745					750
Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly
				755					760					765
Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met
				770					775					780
Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn
				785					790					795
Asn	Gly	Ser	Val	Arg	Thr	Ala								
				800										

<210> 261
 <211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
tcccatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
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gttcgggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150
tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250
agtttttagag aacctagtac gaagtgttcc ctctggggag ccaggtcgtg 300
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350
tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgtttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450
 gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccctattc 500
 tggtcgatca aaccaaaca tgtttccatt gttttgcatg cagaggaacc 550
 ttatatgaa aatgaagagc cagagccaga gccggagcca gctgcaaac 600
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 ccatatgta cctcatacaa gtcacctgtc accacttttag ataagagcac 700
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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
1				5					10					15

Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45

Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Pro Lys His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys		
65	70	75
Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu		
80	85	90
Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly		
95	100	105
Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro		
110	115	120
Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala		
125	130	135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu		
140	145	150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val		
155	160	165
Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro		
170	175	180
Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu		
185	190	195
Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys		
200	205	210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp		
215	220	225
Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala		
230	235	240
Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu		
245	250	255
Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala		
260	265	270
Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro		
275	280	285
Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile		
290	295	300
Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp		
305	310	315
Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val		
320	325	330
Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala		
335	340	345

Leu Leu Lys Val Tyr
350

<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

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gaccgggcaa gtttgtccag gccttggtgg gggaggacgc cgtgttctcc 250
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 caaattaaac taaacaatat atttaaagat gatataaac tactcagtgt 2300
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 aaa 2403

<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

Met	Ala	Phe	Val	Leu	Ile	Leu	Val	Leu	Ser	Phe	Tyr	Glu	Leu	Val
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Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

	20	25	30
Leu Val Gly Glu Asp	Ala Val Phe Ser Cys	Ser Leu Phe Pro Glu	
	35	40	45
Thr Ser Ala Glu Ala	Met Glu Val Arg Phe	Phe Arg Asn Gln Phe	
	50	55	60
His Ala Val Val His	Leu Tyr Arg Asp Gly	Glu Asp Trp Glu Ser	
	65	70	75
Lys Gln Met Pro Gln	Tyr Arg Gly Arg Thr	Glu Phe Val Lys Asp	
	80	85	90
Ser Ile Ala Gly Gly	Arg Val Ser Leu Arg	Leu Lys Asn Ile Thr	
	95	100	105
Pro Ser Asp Ile Gly	Leu Tyr Gly Cys Trp	Phe Ser Ser Gln Ile	
	110	115	120
Tyr Asp Glu Glu Ala	Thr Trp Glu Leu Arg	Val Ala Ala Leu Gly	
	125	130	135
Ser Leu Pro Leu Ile	Ser Ile Val Gly Tyr	Val Asp Gly Gly Ile	
	140	145	150
Gln Leu Leu Cys Leu	Ser Ser Gly Trp Phe	Pro Gln Pro Thr Ala	
	155	160	165
Lys Trp Lys Gly Pro	Gln Gly Gln Asp Leu	Ser Ser Asp Ser Arg	
	170	175	180
Ala Asn Ala Asp Gly	Tyr Ser Leu Tyr Asp	Val Glu Ile Ser Ile	
	185	190	195
Ile Val Gln Glu Asn	Ala Gly Ser Ile Leu	Cys Ser Ile His Leu	
	200	205	210
Ala Glu Gln Ser His	Glu Val Glu Ser Lys	Val Leu Ile Gly Glu	
	215	220	225
Thr Phe Phe Gln Pro	Ser Pro Trp Arg Leu	Ala Ser Ile Leu Leu	
	230	235	240
Gly Leu Leu Cys Gly	Ala Leu Cys Gly Val	Val Met Gly Met Ile	
	245	250	255
Ile Val Phe Phe Lys	Ser Lys Gly Lys Ile	Gln Ala Glu Leu Asp	
	260	265	270
Trp Arg Arg Lys His	Gly Gln Ala Glu Leu	Arg Asp Ala Arg Lys	
	275	280	285
His Ala Val Glu Val	Thr Leu Asp Pro Glu	Thr Ala His Pro Lys	
	290	295	300
Leu Cys Val Ser Asp	Leu Lys Thr Val Thr	His Arg Lys Ala Pro	
	305	310	315

Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val	320	325	330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val	335	340	345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp	350	355	360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn	365	370	375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr	380	385	390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr	395	400	405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe	410	415	420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys	425	430	435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr	440	445	450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp	455	460	465

Gly

<210> 268
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<400> 268
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 tggtgagggc taggaaaaga gtttgttggg aaccctgggt tatcggcctc 100
 gtcattcttca tatccctgat tgcctggca gtgtgcattg gactcactgt 150
 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
 tgtcattttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
 attttataaa tctccattaa gggaagaatt tgtcaagtct caggttatca 350
 agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400
 agatttcact ctactgagga tcttgaaact gtagataaaa ttgttcaact 450
 tgttttacat gaaaagctgc aagatgctgt aggacccct aaagtagatc 500

ctcaactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat 550
 ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600
 caggatcggt ggtgggacag aagtagaaga ggggtgaatgg ccctggcagg 650
 ctagcctgca gtgggatggg agtcatcgct gtggagcaac cttaattaat 700
 gccacatggc ttgtgagtgc tgctcactgt tttacaacat ataagaacct 750
 tgccagatgg actgcttcct ttggagtaac aataaaacct tcgaaaatga 800
 aacggggtct ccggagaata attgtccatg aaaaatacaa acacccatca 850
 catgactatg atatttctct tgcagagctt tctagccctg ttccctacac 900
 aaatgcagta catagagttt gtctccctga tgcctcctat gagtttcaac 950
 caggatgatg gatgtttgtg acaggatttg gagcactgaa aaatgatggg 1000
 tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac 1050
 aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt 1100
 tatgtgctgg ctcccttagaa ggaaaaacag atgcatgcca gggtgactct 1150
 ggaggaccac tgggttagttc agatgctaga gatctctggg accttgctgg 1200
 aatagtgagc tggggagatg aatgtgcgaa acccaacaag cctgggtgtt 1250
 atactagagt tacggccttg cgggactgga ttacttcaaa aactggatc 1300
 taagagacaa aagcctcatg gaacagataa catttttttt tgttttttgg 1350
 gtgtggaggc cttttttaga gatacagaat tggagaagac ttgcaaaaca 1400
 gctagatttg actgatctca ataaactgtt tgcttgatgc atgtattttc 1450
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 atacaatatt acattacagc ctgtattcat ttgttctcta gaagttttgt 1600
 cagaattttg acttggtgac ataaatttgt aatgcatata tacaatttga 1650
 agcactcctt ttcttcagtt cctcagctcc tctcatttca gcaaatatcc 1700
 attttcaagg tgcagaacaa ggagtgaag aaaatataag aagaaaaaaa 1750
 tcccctacat ttatttggca cagaaaagta ttaggtgttt ttcttagtgg 1800
 aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag 1850
 aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag 1900
 tccagaaaga agccaagata tatccttatt ttcatttcca aacaactact 1950

atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata 2000
 caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050
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 cca 2103

<210> 269
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 269
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 Trp Glu Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile
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 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
 35 40 45
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
 50 55 60
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
 65 70 75
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
 80 85 90
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
 95 100 105
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
 110 115 120
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
 125 130 135
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
 140 145 150
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
 155 160 165
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
 170 175 180
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
 185 190 195
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
 200 205 210
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
 215 220 225

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro
				230					235				240	
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys
				245					250				255	
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys
				260					265				270	
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser
				275					280				285	
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp
				290					295				300	
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly
				305					310				315	
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg
				320					325				330	
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro
				335					340				345	
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly
				350					355				360	
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly
				365					370				375	
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly
				380					385				390	
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly
				395					400				405	
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys
				410					415				420	

Thr Gly Ile

<210> 270
 <211> 1170
 <212> DNA
 <213> Homo sapiens

<400> 270
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 cagacgtcag ctggtggatt cccgctgcat caaggcctac ccaactgtctc 150
 catgctgggc tctccctgcc ttctgtggct cctggccgtg accttcttgg 200
 ttcccagagc tcagcccttg gccctcaag actttgaaga agaggaggca 250

gatgagactg agacggcgtg gccgcctttg ccggctgtcc cctgcgacta 300
cgaccactgc cgacacctgc aggtgccctg caaggagcta cagagggtcg 350
ggccggcggc ctgcctgtgc ccaggactct ccagccccgc ccagccgccc 400
gacccgcccgc gcatgggaga agtgcgcatt gcggccgaag agggccgcgc 450
agtgtccac tgggtgtgcc ccttctcccc ggtcctccac tactggctgc 500
tgctttggga cggcagcgag gctgcgaga aggggcccc gctgaacgct 550
acgggtccgca gagccgaact gaaggggctg aagccagggg gcatttatgt 600
cgtttgcgta gtggccgcta acgaggccgg ggcaagccgc gtgccccagg 650
ctggaggaga gggcctcgag ggggccgaca tccctgcctt cgggccttgc 700
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cgggggtgggc acggccctgg ccctgctaag ctgtgccgcc ctggtgtggc 800
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gccgcagggg cgctctgaaa ggggcctggg ggcatctcgg gcacagacag 900
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cctccagggg gggctggacg gcgagctggg agccagcccc aggtccagg 1000
gccacggcgg agtcatggtt ctcaggactg agcgcttgtt taggtccggt 1050
acttggcgct ttgtttcctg gctgaggtct gggaaggaat agaaaggggc 1100
ccccaatttt tttttaagcg gccagataat aaataatgta acctttgcgg 1150
ttaaaaaaaaa aaaaaaaaaa 1170

<210> 271
<211> 238
<212> PRT
<213> Homo sapiens

<400> 271
Met Leu Gly Ser Pro Cys Leu Leu Trp Leu Leu Ala Val Thr Phe
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Leu Val Pro Arg Ala Gln Pro Leu Ala Pro Gln Asp Phe Glu Glu
20 25 30
Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala
35 40 45
Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys
50 55 60
Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly
65 70 75

Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	
				80					85					90	
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	
				95					100					105	
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	
				110					115					120	
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	
				125					130					135	
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	
				140					145					150	
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	
				155					160					165	
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	
				170					175					180	
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	
				185					190					195	
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	
				200					205					210	
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	
				215					220					225	
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			
				230					235						

<210> 272
 <211> 2397
 <212> DNA
 <213> Homo sapiens

<400> 272
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 tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200
 gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgctgtctct 250
 acgccctcaa tctgctcttt tggttaatgt ccatcagtggt gttggcagtt 300
 tctgcttgga tgagggacta cctaaataat gttctcactt taactgcaga 350
 aacgagggta gaggaagcag tcattttgac ttactttcct gtgggttcac 400
 cggtcagat tgctgtttgc tgtttcctta tcattgtggg gatgttagga 450
 tattgtggaa cggtgaaaag aaatctgttg cttcttgcat ggtactttgg 500

aagtttgctt gtcattttct gtgtagaact ggcttggtgc gtttgacat 550
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aaagccagga tgacaaatta tggattacct agatatcggt ggcttactca 650
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tgtgttagag aattcccagg atgttccaaa caggcccacc aggaagatct 800
cagtgcctt tatcaagagg gttgtgggaa gaaaatgtat tcctttttga 850
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caaacttggt ttattggact tgtgaatttt tgagtacata ctatgtgttt 1200
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tactattcta tgctttaaaa tgaggatgga aaagtttcat gtcataagtc 1300
accacctgga caataattga tgcccttaaa atgctgaaga cagatgtcat 1350
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aggcagcatg gtttgattag catttccgca tccatgcaaa cgagtcacat 1450
atggtgggac tggagccata gtaaagggtg atttacttct accaactagt 1500
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acttttatta ctacgcgatc tattcttctg atgctaaata aattatatat 1600
cagaaaactt tcaatattgg tgactacct aatgtgattt ttgctgggta 1650
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tgatcaggga ttttttgat ataagtotgt gttaaactctg tataattcag 1750
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ttgtcctgta tagcatcatt atttttagcc tttcctgtta ataaagcttt 1850
actattctgt cctgggctta tattacacat ataactgtta tttaaatact 1900
taaccactaa ttttgaaaat taccagtgtg atacatagga atcattattc 1950


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agaatgtagt ctggtcttta ggaagtatta ataagaaaat ttgcacataa 2000
cttagttgat tcagaaagga cttgtatgct gtttttctcc caaatgaaga 2050
ctctttttga cactaaacac tttttaaaaa gcttatcttt gccttctcca 2100
aacaagaagc aatagtctcc aagtcaatat aaattctaca gaaaatagtg 2150
ttctttttct ccagaaaaat gcttgtgaga atcattaaaa catgtgacaa 2200
tttagagatt ctttgtttta tttcactgat taatatactg tggcaaatta 2250
cacagattat taaatTTTTT tacaagagta tagtatattt atttgaaatg 2300
ggaaaagtgc attttactgt attttgtgta ttttgtttat ttctcagaat 2350
atggaaagaa aattaaaatg tgtcaataaa tattttctag agagtaa 2397

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<210> 273
<211> 305
<212> PRT
<213> Homo sapiens

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<400> 273
Met Ala Arg Glu Asp Ser Val Lys Cys Leu Arg Cys Leu Leu Tyr
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Ala Leu Asn Leu Leu Phe Trp Leu Met Ser Ile Ser Val Leu Ala
             20             25             30
Val Ser Ala Trp Met Arg Asp Tyr Leu Asn Asn Val Leu Thr Leu
             35             40             45
Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe
             50             55             60
Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile
             65             70             75
Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu
             80             85             90
Leu Leu Leu Ala Trp Tyr Phe Gly Ser Leu Leu Val Ile Phe Cys
             95            100            105
Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met
            110            115            120
Val Pro Val Gln Trp Ser Asp Met Val Thr Leu Lys Ala Arg Met
            125            130            135
Thr Asn Tyr Gly Leu Pro Arg Tyr Arg Trp Leu Thr His Ala Trp
            140            145            150
Asn Phe Phe Gln Arg Glu Phe Lys Cys Cys Gly Val Val Tyr Phe
            155            160            165
Thr Asp Trp Leu Glu Met Thr Glu Met Asp Trp Pro Pro Asp Ser

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170					175					180				
Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln
				185					190					195
Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met
				200					205					210
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe
				215					220					225
Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu
				230					235					240
Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro
				245					250					255
Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His
				260					265					270
Leu	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg
				275					280					285
Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe
				290					295					300
Glu	Met	Glu	Glu	Leu										
				305										

<210> 274
 <211> 2063
 <212> DNA
 <213> Homo sapiens

<400> 274
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 ttctgacctg ctggccagcc aggacctgtg tggggaggcc ctctgtctgc 150
 cttgggtga caatctcagc tccaggctac agggagaccg ggaggatcac 200
 agagccagca tggtacagga tcctgacagt gatcaacctc tgaacagcct 250
 cgatgtcaaa cccctgcgca aaccccgat ccccatggag accttcagaa 300
 aggtggggat ccccatcatc atagcactac tgagcctggc gagtatcatc 350
 attgtggttg tcctcatcaa ggtgattctg gataaatact acttcctctg 400
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 tggactgtcc cttgggggag gacgaggagc actgtgtcaa gagcttcccc 500
 gaagggcctg cagtggcagt ccgcctctcc aaggaccgat ccacactgca 550
 ggtgctggac tcggccacag ggaactggtt ctctgcctgt ttcgacaact 600

tcacagaagc tctcgctgag acagcctgta ggcagatggg ctacagcaga 650
 gctgtggaga ttggcccaga ccaggatctg gatgttggtg aaatcacaga 700
 aaacagccag gagcttcgca tgcggaactc aagtgggccc tgtctctcag 750
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 acccccactg ggtcctcaag gcagcccact gcttcaggaa acataccgat 950
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 ccaagacaa tgacatcgcc ctcatgaagc tgcagttccc actcactttc 1100
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 gagggagat gtctgacata ctgctgcagg cgtcagtcca ggtcattgac 1250
 agcacacggt gcaatgcaga cgatgcgtac cagggggaag tcaccgagaa 1300
 gatgatgtgt gcaggcatcc cggaaggggg tgtggacacc tgccagggtg 1350
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 ggcctcaatt cctgtaagag accctcgag cccagaggcg cccagaggaa 1700
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 agacacagcc cactgaacaa ggtctcaggg gtattgctaa gccaagaagg 1800
 aactttccca cactactgaa tggaagcagg ctgtcttgta aaagcccaga 1850
 tcaactgtgg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg 1900
 tcttcaccca tccccaagcc tactagagca agaaaccagt tgtaataata 1950
 aatgcactgc cctactgttg gtatgactac cgttacctac tgttgtcatt 2000
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caaaaaaaaaaaa aaa 2063

<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

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Val	Lys	Pro	Leu	Arg	Lys	Pro	Arg	Ile	Pro	Met	Glu	Thr	Phe	Arg
				20					25					30
Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser
				35					40					45
Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr
				50					55					60
Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln
				65					70					75
Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu
				80					85					90
His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg
				95					100					105
Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr
				110					115					120
Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu
				125					130					135
Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu
				140					145					150
Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn
				155					160					165
Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser
				170					175					180
Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu
				185					190					195
Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser
				200					205					210
Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys
				215					220					225
Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His
				230					235					240
Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala
				245					250					255

265

Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala	Val	Ala	Lys	
				260					265					270	
Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro	Met	Tyr	Pro	Lys	Asp	Asn	Asp	
				275					280					285	
Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly	Thr	
				290					295					300	
Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Phe	Asp	Glu	Glu	Leu	Thr	Pro	
				305					310					315	
Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn	
				320					325					330	
Gly	Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val	
				335					340					345	
Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu	
				350					355					360	
Val	Thr	Glu	Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val	
				365					370					375	
Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser	
				380					385					390	
Asp	Gln	Trp	His	Val	Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys	
				395					400					405	
Gly	Gly	Pro	Ser	Thr	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr	
				410					415					420	
Leu	Asn	Trp	Ile	Tyr	Asn	Val	Trp	Lys	Ala	Glu	Leu				
				425					430						

<210> 276
 <211> 3143
 <212> DNA
 <213> Homo sapiens

<400> 276
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 ttttcctctt ccaactgctt cagctgctgc tgccgacgac gaccgcgggg 200
 ggaggcgggc agggggccat gccaggggtc agatactatg caggggatga 250
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 ctctgctcct gagtggatgat ggaaatactc tctacgtggg ggctcgagaa 350
 gccattctgg ccttggatat ccaggatcca ggggtcccca ggctaaagaa 400

catgataccg tggccagcca gtgacagaaa aaagagtga tgtgccttta 450
agaagaagag caatgagaca cagtgtttca acttcatccg tgccttggtt 500
tcttacaatg tcacccatct ctacacctgc ggcaccttcg ccttcagccc 550
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aagcatacgg ctgtcttggt ggatgggatg ctctattctg gtactatgaa 700
caacttcctg ggcagtgagc ccatcctgat gcgcacactg ggatcccagc 750
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ccctcctctg ataaggccct gaccttcatg aaggaccatt tcctgatgga 1300
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 agaagcctct tccactgtct acaatggctc cctcttgctg atagtgcagg 1950
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 ttcagggtg tgagaccctg cgccctgggg agaaggcccc gttaagcaga 2300
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 caggggtaat ctgagccttc ttcactcctt taccctagct gaccttca 3050
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 agagactgtt tttttttat taaaaatata aggcttaaaa aaa 3143

<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

Met	Ala	Leu	Pro	Ala	Leu	Gly	Leu	Asp	Pro	Trp	Ser	Leu	Leu	Gly	
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Leu	Phe	Leu	Phe	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Pro	Thr	Thr	Thr	
				20					25					30	
Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	
				35					40					45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	
				50					55					60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	
				65					70					75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	
				80					85					90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	
				95					100					105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	
				110					115					120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	
				125					130					135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	
				140					145					150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	
				155					160					165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	
				170					175					180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	
				185					190					195	
Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg	
				200					205					210	
Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg	
				215					220					225	
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr	
				230					235					240	
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp	
				245					250					255	
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	
				260					265					270	
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr	
				275					280					285	
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro	

290										295					300				
Phe	Asn	Val	Ile	Arg	His	Ala	Val	Leu	Leu	Pro	Ala	Asp	Ser	Pro					
				305					310					315					
Thr	Ala	Pro	His	Ile	Tyr	Ala	Val	Phe	Thr	Ser	Gln	Trp	Gln	Val					
				320					325					330					
Gly	Gly	Thr	Arg	Ser	Ser	Ala	Val	Cys	Ala	Phe	Ser	Leu	Leu	Asp					
				335					340					345					
Ile	Glu	Arg	Val	Phe	Lys	Gly	Lys	Tyr	Lys	Glu	Leu	Asn	Lys	Glu					
				350					355					360					
Thr	Ser	Arg	Trp	Thr	Thr	Tyr	Arg	Gly	Pro	Glu	Thr	Asn	Pro	Arg					
				365					370					375					
Pro	Gly	Ser	Cys	Ser	Val	Gly	Pro	Ser	Ser	Asp	Lys	Ala	Leu	Thr					
				380					385					390					
Phe	Met	Lys	Asp	His	Phe	Leu	Met	Asp	Glu	Gln	Val	Val	Gly	Thr					
				395					400					405					
Pro	Leu	Leu	Val	Lys	Ser	Gly	Val	Glu	Tyr	Thr	Arg	Leu	Ala	Val					
				410					415					420					
Glu	Thr	Ala	Gln	Gly	Leu	Asp	Gly	His	Ser	His	Leu	Val	Met	Tyr					
				425					430					435					
Leu	Gly	Thr	Thr	Thr	Gly	Ser	Leu	His	Lys	Ala	Val	Val	Ser	Gly					
				440					445					450					
Asp	Ser	Ser	Ala	His	Leu	Val	Glu	Glu	Ile	Gln	Leu	Phe	Pro	Asp					
				455					460					465					
Pro	Glu	Pro	Val	Arg	Asn	Leu	Gln	Leu	Ala	Pro	Thr	Gln	Gly	Ala					
				470					475					480					
Val	Phe	Val	Gly	Phe	Ser	Gly	Gly	Val	Trp	Arg	Val	Pro	Arg	Ala					
				485					490					495					
Asn	Cys	Ser	Val	Tyr	Glu	Ser	Cys	Val	Asp	Cys	Val	Leu	Ala	Arg					
				500					505					510					
Asp	Pro	His	Cys	Ala	Trp	Asp	Pro	Glu	Ser	Arg	Thr	Cys	Cys	Leu					
				515					520					525					
Leu	Ser	Ala	Pro	Asn	Leu	Asn	Ser	Trp	Lys	Gln	Asp	Met	Glu	Arg					
				530					535					540					
Gly	Asn	Pro	Glu	Trp	Ala	Cys	Ala	Ser	Gly	Pro	Met	Ser	Arg	Ser					
				545					550					555					
Leu	Arg	Pro	Gln	Ser	Arg	Pro	Gln	Ile	Ile	Lys	Glu	Val	Leu	Ala					
				560					565					570					
Val	Pro	Asn	Ser	Ile	Leu	Glu	Leu	Pro	Cys	Pro	His	Leu	Ser	Ala					
				575					580					585					

Leu	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu	590	595	600
Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln	605	610	615
Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly	620	625	630
Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln	635	640	645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His	650	655	660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala	665	670	675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu	680	685	690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser	695	700	705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu	710	715	720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His	725	730	735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp	740	745	750
Ala	Asp	Asn	Asn	Cys	Leu	Gly	Thr	Glu	Val	Ala					755	760	

<210> 278
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 278
 ctgctggtga aatctggcgt ggag 24

<210> 279
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 279
gtctgtgcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
catcttgtca tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

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atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200
ttcttcaaga tcacgggtcat aatgtcacca tgcttaacca caaaagaggt 250
ccttttatgc cagattttaa aaaggaagaa aaatcatatc aagttatcag 300
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
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ggatatcatg gattccttaa agaatgagaa cttcgacatg gtgatagtgtg 500
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 ccagcctcca tgtccagacc tagtcagcct ctctcactcc tgcccctact 2050
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 ttctgttttg ttctcccaca tattctcttc aatgctcagg aagcctgccc 2150
 tgtgcttgag agttcagggc cggacacagg ctacaggtc tccacattgg 2200
 gtccctgtct ctggtgcca cagtgaagctc cttcttgggt gagcaggcat 2250
 ggagactgta ggtttccaga tttcctgaaa aataaaagtt tacagcgta 2300
 tctctcccca acctcaacta 2320

<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282

Met	Ala	Gly	Gln	Arg	Val	Leu	Leu	Leu	Val	Gly	Phe	Leu	Leu	Pro
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Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile
				155					160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
				170					175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
				185					190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
				200					205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
				215					220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
				230					235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
				245					250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly

260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn	
275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu	
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu	
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys	
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp	Val His Leu Ala Ala Asn	
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His	
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile	
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro	Met Val Gly Ile Pro Leu	
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys	
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu	
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser	
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser	
440	445	450
Pro Thr Gln Arg Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr	
455	460	465
Gly Gly Ala Thr His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp	
470	475	480
His Glu Gln Tyr Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu	
485	490	495
Thr Leu Gly Thr Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala	
500	505	510
Val Trp Trp Leu Arg Gly Ala Arg Lys	Val Lys Glu Thr	
515	520	

<210> 283
 <211> 24
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 283
tgcctttgct cacctacccc aagg 24

<210> 284
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 284
tcaggctggt ctccaaagag aggg 24

<210> 285
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 285
cccaaagatg tccacctggc tgcaaattgtg aaaattgtgg actgg 45

<210> 286
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 286
gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50
ggttgagggg ctgcctctgg catatgcaca cactcacaca ttctgtcaca 100
cccgtcacac acacatacca tgtttctccat ccccccaggt ccagccctca 150
gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200
cgtccagtgg gcaggcggct tcatccctcc tttctotccc aaagcccaac 250
tgctgtcact gcatgctctg ccaaggagga ggggaactgca gtgacagcag 300
gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350
gttcagcgag cctagagagg gcagactatc aggggtgccgg cggtgagaat 400
ccagggagag gagcggaaac agaagagggg cagaagaccg gggcacttgt 450

gggttgcaga gccctcagc catgttggga gccaaagccac actggctacc 500
 aggtccccta cacagtcccg ggctgccott ggttctggtg cttctggccc 550
 tgggggccgg gtgggccag gaggggtcag agcccgctct gctggagggg 600
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 tactcaagtt tctctggctt cctcatcttc cctctctgag gacccaagtc 1100
 tttcaagcac aagaatccag cccctgacaa ctttcttctg ccctctcttg 1150
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 cctctttgca tgggaccctg tgccaaacac ccaagttaa gagaagagta 1250
 gagctgtggc atctccagac caggccttcc caccaccca ccccagtta 1300
 cctcccagc cacctgctgc atctgttctt gcctgcagcc ctaggatcag 1350
 ggcaagggtt ggcaagaagg aagatctgca ctactttgcg gcctctgctc 1400
 ctccggttcc cccaccccag cttcctgctc aatgctgac agggacaggt 1450
 ggcgcaggtg agcctgacag gccccacag gagcccagat ggacaagcct 1500
 cagcgtaccc tgcaggcttc ttctgtgag gaaagccagc atcacggatc 1550
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ccacctcctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950
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 cattccttca gacctctcc tgccagtatg ctaaaccctc cctctctctt 2150
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 caactagaga atggtgggtca gtgagacact atagaattac taaggagaag 2250
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 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
1				5					10					15
Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

170	175	180
Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser		
185	190	195
Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu		
200	205	

<210> 288
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 288
 aggcagccac cagctctgtg ctac 24

<210> 289
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

<400> 289
 cagagaggga agatgaggaa gccagag 27

<210> 290
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-42
 <223> Synthetic construct.

<400> 290
 ctgtgctact gcccttgac cctggggacc gagtgtctct gc 42

<210> 291
 <211> 1570
 <212> DNA
 <213> Homo sapiens

<400> 291
 gctgtttctc tcgcgccacc actggcggcc ggccgcagct ccaggtgtcc 50
 tagccgcccc gcctcgacgc cgtcccggga cccctgtgct ctgcgcgaag 100
 ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150

ttccccgcggg gccgtgactg ggcgggcttc agccatgaag accctcatag 200
 ccgcctactc cggggctcctg cgcgggcgagc gtcaggccga ggctgaccgg 250
 agccagcgct ctcaoggagg acctgcgctg tcgcgcgagg ggtctgggag 300
 atggggcact ggatccagca tcctctccgc cctccaggac ctcttctctg 350
 tcacctgggt caataggtcc aagggtgaaa agcagctaca ggtcatctca 400
 gtgctccagt gggctcctgtc ctctcttgta ctgggagtgg cctgcagtgc 450
 catcctcatg tacatattct gcactgattg ctgggtcatc gctgtgctct 500
 acttcacttg gctgggtgtt gactggaaca cacccaagaa aggtggcagg 550
 aggtcacagt ggggtccgaaa ctgggctgtg tggcgctact ttcgagacta 600
 ctttcccatc cagctgggtga agacacacaa cctgctgacc accagggaact 650
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 aacttcagca cagaggccac agaagtgagc aagaagttcc caggcatacg 750
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 ctgggttcca tctactcctt tggagagaat gaagtgtaca agcaggtgat 1050
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 cacaagacca agttcggcct cccggagact gaggtcctgg aggtgaactg 1350
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 tttgctctgt aaatttgaa gtgtcatggg tgtctgtggg ttatttaaaa 1450
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1550
 aaaaaaaaaa aaaaaaaaaa 1570

<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu
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Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro
				20					25					30
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser
				35					40					45
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn
				50					55					60
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln
				65					70					75
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile
				80					85					90
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu
				95					100					105
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly
				110					115					120
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr
				125					130					135
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu
				140					145					150
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile
				155					160					165
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu
				170					175					180
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu
				185					190					195
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser
				200					205					210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu
				215					220					225
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
				230					235					240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr
				245					250					255
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly

	260		265		270
Ala Asp Leu Val	Pro Ile Tyr Ser Phe	Gly Glu Asn Glu Val	Tyr		
	275	280	285		
Lys Gln Val Ile	Phe Glu Glu Gly Ser	Trp Gly Arg Trp Val	Gln		
	290	295	300		
Lys Lys Phe Gln	Lys Tyr Ile Gly Phe	Ala Pro Cys Ile Phe	His		
	305	310	315		
Gly Arg Gly Leu	Phe Ser Ser Asp Thr	Trp Gly Leu Val Pro	Tyr		
	320	325	330		
Ser Lys Pro Ile	Thr Thr Val Val Gly	Glu Pro Ile Thr Ile	Pro		
	335	340	345		
Lys Leu Glu His	Pro Thr Gln Gln Asp	Ile Asp Leu Tyr His	Thr		
	350	355	360		
Met Tyr Met Glu	Ala Leu Val Lys Leu	Phe Asp Lys His Lys	Thr		
	365	370	375		
Lys Phe Gly Leu	Pro Glu Thr Glu Val	Leu Glu Val Asn			
	380	385			

<210> 293
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 293
 gctgacctgg ttcccatcta ctcc 24

<210> 294
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 294
 cccacagaca cccatgacac ttcc 24

<210> 295
 <211> 50
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
gggcggcggg atggggggccg ggggcggcgg gcgcgcgact cgctgaggcc 50
ccgacgcagg gccggggccgg gccagggcc gaggagcgcg gcggccagag 100
cgggggccgcg gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200
ggctctgctg accttgtgcc ttggacggct gtcctcagcg aggggccgtg 250
caccgcctcc tgagcagcgc catgggcctg ctggccttcc tgaagaccca 300
gttcgtgctg cacctgctgg tcggctttgt cttcgtggcg agtggctctg 350
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cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450
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cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550
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 cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950
 aacottcaac tgtaattatt ggacttttga gtcttagatg gtcctgacct 2000
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ttgttctgtt gccaggctg gactacagt gcacagtctt ggctcactgc 2650
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 aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gcccacta 2950
 ccaggagagac tgaagtggga ggatcgcttg ggcattgagaa gtcgaggctg 3000
 cagtgagtcg aggttgtgcg actgcattcc agcctggaca acagagttag 3050
 accctgtctc 3060

<210> 297
 <211> 368
 <212> PRT
 <213> Homo sapiens

<400> 297
 Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu
 1 5 10 15
 Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe
 20 25 30
 Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu
 35 40 45
 Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln
 50 55 60
 Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu
 65 70 75
 Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala
 80 85 90
 Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly
 95 100 105
 Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val
 110 115 120
 Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr
 125 130 135
 Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu
 140 145 150
 Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr
 155 160 165

Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe	
				170					175					180	
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys	
				185					190					195	
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	
				200					205					210	
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val	
				215					220					225	
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	
				230					235					240	
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	
				245					250					255	
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	
				260					265					270	
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	
				275					280					285	
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	
				290					295					300	
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	
				305					310					315	
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	
				320					325					330	
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	
				335					340					345	
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu	
				350					355					360	
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln								
				365											

<210> 298
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 298
 cttcctctgt gggtaggacca tgtg 24

<210> 299
 <211> 21
 <212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

gccacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggtcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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tgctcctgggg cagccaccag gcatattcat ctttgtgtgt gtttttcttt 100

tgcttttagca ctggggcact tcttgcttat ttctttggta ggaaaggggc 150

tcagtttgtc ttgtgggggt ggtggcaggc aggcgggctt acgcctgata 200

cgccctggg ttagaaggga agggaagata aacttttata caaatgggga 250

tagctgggggt ctgagacctg ctctctcagt aaaattcctg ggatctgcct 300

ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350

ttctctctgt tcttaggatc aaagtattta gagctacaag agccctcatg 400

gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450

tgtcgttcct gtaatgtggt atgccatggg gtctttgcac aagcctttcc 500

tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550

atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600

ctggcctgac agaattctcat cttgtttaat gctctcataa gaccacttgt 650

ttcccttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700

gttgatatggg ttgtgtctgt tccccagaat gccagctct gagctgcgtg 750

aggggtcaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850
 aaatctctca gttcaccaga tgggtgtaggg cccagcattg taaattcaca 900
 cgttgactgt gcttgtgaat tatctgggga tgcaggtcct gattcagtag 950
 gcccagggtg ggcatctcta acaaactccc acgtgatgct gatgctggtc 1000
 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050
 tggctcacac ctatgatccc agcactttgg gaggctgagg caggctgata 1100
 acctggagtc aggatttcaa gactagcctg gccaacatgg tggaacccca 1150
 tctgtactaa aaatacaca attagctggg catggtggca catgcctgta 1200
 gtcccagcta cttgggaggg tgaagcaaga gaatcgcttg aacctgggag 1250
 gcggagggtg cagtgaagcc agatcaggcc actgtattcc aaccagggtg 1300
 acagagtggg actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
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His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
				20					25					30
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35					40					45
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50					55					60
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
				65					70					75
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr
				80					85					90
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln
				95					100					105
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu
				110					115					120
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr
				125					130					135
Cys	Gly	Val	Leu	Leu	Ser	Phe	Leu							

<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

<400> 303
 ggctggactg gaactcctgg tccaagtga tccaccogcc tcagcctccc 50
 aagggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100
 tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150
 tatgctgtgg tggctagtgc tctactcct acctacatta aaatctgttt 200
 tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250
 ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300
 ttctacccac accgtcccct cgaagccggg gacagcctca ccttgcctggc 350
 ctctcgctgg agcagtgcc tcaccaactg tctcacgtct ggaggcactg 400
 actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450
 tgggccttgc cctggccgta gaagggattg acaagcccga agatttcata 500
 ggcgatggct cccactgccc aggcacacgc cttgctgtag tcaatcactg 550
 ccctggggcc aggacgggccc gtggacacct gctcagaagc agtgggtgag 600
 acatcacgct gcccgcccat ctaacctttt catgtcctgc acatcacctg 650
 atccatgggc taatctgaac tctgtcccaa ggaaccacaga gcttgagtga 700
 gctgtggctc agaccacaga ggggtctgct tagaccacct ggtttatgtg 750
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 gtggcagggg aggaacttgt gccaaattat gggtcagaaa agatggaggt 850
 gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg 900
 ggaagggctg ccgatggcgc atgacacact cgggactcac ctctggggcc 950
 atcagacagc cgtttccgcc ccgatccacg taccagctgc tgaagggcaa 1000
 ctgcaggccg atgctctcat cagccaggca gcagccaaaa tctgcgatca 1050
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 ctcccctcct tccctctgag aggccctcct atgtccctac taaagccacc 1150
 agcaagacat agctgacagg ggctaattgg tcagtgttgg ccaggaggt 1200
 cagcaaggcc tgagagctga tcagaagggc ctgctgtgcg aacacggaaa 1250

tgcctccagt aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg 1300
 ctcaatttaa atcatgttct agtaattgga gctgtcccca agaccaaagg 1350
 agctagagct tggttcaa at gatctccaag ggccttata cccaggaga 1400
 ctttgatttg aatttgaaac cccaaatcca aacctaagaa ccaggtgcat 1450
 taagaatcag ttattgccgg gtgtggtggc ctgtaatgcc aacattttgg 1500
 gaggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg 1550
 gccaacatgg tgaaaccctt gtctctacta aaaatacaaa aaaactagcc 1600
 aggcattgtg gtgtgtgcct gtatcccagc tactcgggag gctgagacag 1650
 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700
 ttcagcctga gcaacacagc gagactctgt ctcagaaaaa ataaaaaaag 1750
 aattatggtt atttgtaa 1768

<210> 304
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 304
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 1 5 10 15
 Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu
 20 25 30
 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly
 35 40 45
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
 50 55 60
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
 65 70 75
 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala
 80 85 90
 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
 95 100 105
 Arg Arg Arg Asp

<210> 305
 <211> 989
 <212> DNA
 <213> Homo sapiens

<400> 305

gcggggccgc gagtccgaga cctgtcccag gagctccagc tcacgtgacc 50
 tgtcactgcc tcccgccgcc tctgtcccgc gccatgaccc agccggtgcc 100
 ccggctctcc gtgcccgcgc cgtgtggcct gggctcagcc gcactgggcg 150
 ccgccttcgc cactggcctc ttctgtggga ggcggtgccc cccatggcga 200
 ggccggcgag agcagtgcct gcttcccccc gaggacagcc gcctgtggca 250
 gtatcttctg agccgctcca tgcgggagca cccggcgctg cgaagcctga 300
 ggctgctgac cctggagcag ccgcaggggg attctatgat gacctgcgag 350
 caggcccagc tcttggccaa cctggcgcggt ctcattcagg ccaagaaggc 400
 gctggacctg ggcaccttca cgggctactc cgccctggcc ctggccctgg 450
 cgctgcccgc ggacgggcgc gtggtgacct gcgaggtgga cgcgcagccc 500
 ccggagctgg gacggcccct gtggaggcag gccgaggcgg agcacaagat 550
 cgacctccgg ctgaagcccg ccttggagac cctggacgag ctgctggcgg 600
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 aactgctccg cctactacga gcgctgcctg cagctgctgc gacccgagg 700
 catctcgcc gtctcagag tctgtggcg cgggaagggtg ctgcaacctc 750
 cgaaagggga cgtggcggcc gagtgtgtgc gaaacctaaa cgaacgcac 800
 cggcgggacg tcaggttcta catcagcctc ctgcccctgg gcgatggact 850
 caccttggcc ttcaagatct agggctggcc cctagttagt gggctcgagg 900
 gagggttgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950
 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

Met	Thr	Gln	Pro	Val	Pro	Arg	Leu	Ser	Val	Pro	Ala	Ala	Leu	Ala
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Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe
			20						25					30

Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35					40					45

Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
				50					55					60

Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu	
				65					70					75	
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	
				80					85					90	
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	
				95					100					105	
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu	
				110					115					120	
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	
				125					130					135	
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	
				140					145					150	
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	
				155					160					165	
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	
				170					175					180	
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	
				185					190					195	
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	
				200					205					210	
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	
				215					220					225	
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	
				230					235					240	
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly	
				245					250					255	
Leu	Thr	Leu	Ala	Phe	Lys	Ile									
				260											

<210> 307

<211> 2272

<212> DNA

<213> Homo sapiens

<400> 307

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ggatggcgcc gtgaagcccc cacccaacaa gtaccccatc tttttctttg 200

gcacacacga aacagccttc ctgggaacca aggacctgtt cccctacgac 250

aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga 300
 agggctgtgg gagatccaga acaaccccc agccagctac agcgcccctc 350
 cgccagtggag ctctccgac agcgaggccc ccgaggccaa ccccgccgac 400
 ggcaagtacg ctgacgagga cgatgaggac cgggggggtca tggccgtcac 450
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 cagacaagag tagcgacaac agtggcctga agaggaagac gcctgcgcta 550
 aagatgtcgg tctcgaaacg agcccgaag gcctccagcg acctggatca 600
 ggccagcgtg tccccatccg aagaggagaa ctcggaagc tcattctgagt 650
 cggagaagac cagcgaccag gacttcacac ctgagaagaa agcagcggtc 700
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 gtcagcctcc gactccgact ccaaggccga ttcggacggg gccaagcctg 800
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actataaacg gttttttaat ga 2272

<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

Met	Pro	His	Ala	Phe	Lys	Pro	Gly	Asp	Leu	Val	Phe	Ala	Lys	Met
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Lys	Gly	Tyr	Pro	His	Trp	Pro	Ala	Arg	Ile	Asp	Asp	Ile	Ala	Asp
				20					25					30
Gly	Ala	Val	Lys	Pro	Pro	Pro	Asn	Lys	Tyr	Pro	Ile	Phe	Phe	Phe
				35					40					45
Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro
				50					55					60
Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys
				65					70					75
Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala
				80					85					90
Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala
				95					100					105
Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp
				110					115					120
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala
				125					130					135
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser

	140		145		150
Asp Asn Ser Gly	Leu Lys Arg Lys Thr	Pro Ala Leu Lys Met	Ser		
	155		160		165
Val Ser Lys Arg	Ala Arg Lys Ala Ser	Ser Asp Leu Asp Gln	Ala		
	170		175		180
Ser Val Ser Pro	Ser Glu Glu Glu Asn	Ser Glu Ser Ser Ser	Glu		
	185		190		195
Ser Glu Lys Thr	Ser Asp Gln Asp Phe	Thr Pro Glu Lys Lys	Ala		
	200		205		210
Ala Val Arg Ala	Pro Arg Arg Gly Pro	Leu Gly Gly Arg Lys	Lys		
	215		220		225
Lys Lys Ala Pro	Ser Ala Ser Asp Ser	Asp Ser Lys Ala Asp	Ser		
	230		235		240
Asp Gly Ala Lys	Pro Glu Pro Val Ala	Met Ala Arg Ser Ala	Ser		
	245		250		255
Ser Ser Ser Ser	Ser Ser Ser Ser Ser	Asp Ser Asp Val Ser	Val		
	260		265		270
Lys Lys Pro Pro	Arg Gly Arg Lys Pro	Ala Glu Lys Pro Leu	Pro		
	275		280		285
Lys Pro Arg Gly	Arg Lys Pro Lys Pro	Glu Arg Pro Pro Ser	Ser		
	290		295		300
Ser Ser Ser Asp	Ser Asp Ser Asp Glu	Val Asp Arg Ile Ser	Glu		
	305		310		315
Trp Lys Arg Arg	Asp Glu Ala Arg Arg	Arg Glu Leu Glu Ala	Arg		
	320		325		330
Arg Arg Arg Glu	Gln Glu Glu Glu Leu	Arg Arg Leu Arg Glu	Gln		
	335		340		345
Glu Lys Glu Glu	Lys Glu Arg Arg Arg	Glu Arg Ala Asp Arg	Gly		
	350		355		360
Glu Ala Glu Arg	Gly Ser Gly Gly Ser	Ser Gly Asp Glu Leu	Arg		
	365		370		375
Glu Asp Asp Glu	Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg	Gly		
	380		385		390
Arg Gly Pro Pro	Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu	Leu		
	395		400		405
Glu Arg Glu Ala	Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser	Ser		
	410		415		420
Thr Glu Pro Ala	Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val	Arg		
	425		430		435

Pro	Glu	Glu	Lys	Gln	Gln	Ala	Lys	Pro	Val	Lys	Val	Glu	Arg	Thr	
				440					445					450	
Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met	Asp	Arg	Lys	Val	Glu	Lys	
				455					460					465	
Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu	Gln	Lys	Leu	His	Ser	
				470					475					480	
Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg	
				485					490					495	
Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser	
				500					505					510	
Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu	Lys	Lys	
				515					520					525	
Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala	Ala	
				530					535					540	
Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile	
				545					550					555	
Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys	
				560					565					570	
Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala	
				575					580					585	
Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala	
				590					595					600	
Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu	
				605					610					615	
Asp	Lys	Glu	His	Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg	
				620					625					630	
Cys	Gly	Ser	Ser	Glu	Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro	
				635					640					645	
Asp	Leu	Asp	Arg	Pro	Gly	Ser	Asp	Arg	Gln	Glu	Arg	Glu	Arg	Ala	
				650					655					660	
Arg	Gly	Asp	Ser	Glu	Ala	Leu	Asp	Glu	Glu	Ser					
				665					670						

<210> 309

<211> 3871

<212> DNA

<213> Homo sapiens

<400> 309

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ttcatcatga atgctaataa agatgaaaga cttaaagcca gaagccaaga 150
 ttttcacctt tttcctgctt tgatgatgct aagcatgacc atgttgtttc 200
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 <211> 777
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro
 50 55 60
 Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu
 65 70 75
 Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

80										85					90				
Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile					
				95					100					105					
Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala					
				110					115					120					
Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu					
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Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala					
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Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu					
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Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg					
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Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met					
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Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly					
				200					205					210					
Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His					
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His	Tyr	Ile	Arg	Thr	Asp	Ile	Ser	Glu	His	Tyr	Trp	Leu	Asn	Gly					
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Ala	Lys	Phe	Ile	Gly	Thr	Phe	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro					
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Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Ser	Ser	Gln	Glu					
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Gly	Ser	Thr	Ser	Asp	Lys	Thr	Ile	Leu	Ser	Arg	Val	Gly	Arg	Val					
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Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Trp					
				290					295					300					
Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Ile	Pro	Gly	Ser					
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Asp	Gly	Ala	Asp	Thr	Tyr	Phe	Asp	Glu	Leu	Gln	Asp	Ile	Tyr	Leu					
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Leu	Pro	Thr	Arg	Asp	Glu	Arg	Asn	Pro	Val	Val	Tyr	Gly	Val	Phe					
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Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr					
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Ser	Met	Ala	Asp	Ile	Arg	Ala	Val	Phe	Asn	Gly	Pro	Tyr	Ala	His					
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300

Lys	Glu	Ser	Ala	Asp	His	Arg	Trp	Val	Gln	Tyr	Asp	Gly	Arg	Ile	380	385	390
Pro	Tyr	Pro	Arg	Pro	Gly	Thr	Cys	Pro	Ser	Lys	Thr	Tyr	Asp	Pro	395	400	405
Leu	Ile	Lys	Ser	Thr	Arg	Asp	Phe	Pro	Asp	Asp	Val	Ile	Ser	Phe	410	415	420
Ile	Lys	Arg	His	Ser	Val	Met	Tyr	Lys	Ser	Val	Tyr	Pro	Val	Ala	425	430	435
Gly	Gly	Pro	Thr	Phe	Lys	Arg	Ile	Asn	Val	Asp	Tyr	Arg	Leu	Thr	440	445	450
Gln	Ile	Val	Val	Asp	His	Val	Ile	Ala	Glu	Asp	Gly	Gln	Tyr	Asp	455	460	465
Val	Met	Phe	Leu	Gly	Thr	Asp	Ile	Gly	Thr	Val	Leu	Lys	Val	Val	470	475	480
Ser	Ile	Ser	Lys	Glu	Lys	Trp	Asn	Met	Glu	Glu	Val	Val	Leu	Glu	485	490	495
Glu	Leu	Gln	Ile	Phe	Lys	His	Ser	Ser	Ile	Ile	Leu	Asn	Met	Glu	500	505	510
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Lys	Ser	Gln	Gln	Ala	Thr	Ile	Lys	Trp	Tyr	Ile	Gln	Arg	Ser	Gly	620	625	630
Asp	Glu	His	Arg	Glu	Glu	Leu	Lys	Pro	Asp	Glu	Arg	Ile	Ile	Lys	635	640	645
Thr	Glu	Tyr	Gly	Leu	Leu	Ile	Arg	Ser	Leu	Gln	Lys	Lys	Asp	Ser	650	655	660
Gly	Met	Tyr	Tyr	Cys	Lys	Ala	Gln	Glu	His	Thr	Phe	Ile	His	Thr			

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Ile Val Lys Leu Thr Leu Asn Val Ile	Glu Asn Glu Gln Met Glu				
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Asn Thr Gln Arg Ala Glu His Glu Glu	Gly Gln Val Lys Asp Leu				
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Leu Ala Glu Ser Arg Leu Arg Tyr Lys	Asp Tyr Ile Gln Ile Leu				
710	715			720	
Ser Ser Pro Asn Phe Ser Leu Asp Gln	Tyr Cys Glu Gln Met Trp				
725	730			735	
His Arg Glu Lys Arg Arg Gln Arg Asn	Lys Gly Gly Pro Lys Trp				
740	745			750	
Lys His Met Gln Glu Met Lys Lys Lys	Arg Asn Arg Arg His His				
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Arg Asp Leu Asp Glu Leu Pro Arg Ala	Val Ala Thr				
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 <213> Artificial

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 <223> Synthetic construct.

<400> 311
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 <212> DNA
 <213> Artificial

<220>
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 <222> 1-24
 <223> Synthetic construct.

<400> 312
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<210> 313
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 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

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<210> 314
<211> 3934
<212> DNA
<213> Homo sapiens

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<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

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Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu		20	25	30
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala		35	40	45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg		50	55	60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu		65	70	75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala		80	85	90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser		95	100	105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp		110	115	120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu		125	130	135
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro		140	145	150
Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp		155	160	165
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu		170	175	180
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu		185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser		200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu		215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln		230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu		245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly		260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu		275	280	285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu		290	295	300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala				

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Pro Thr Ser Val	Leu Asp Gly Pro Pro	Ala Pro Val Leu Pro	Gly		
	320		325		330
Asp Lys Ala Leu	Asp Phe Pro Gly Phe	Leu Asp Met Met Ala	Pro		
	335		340		345
Arg Leu Arg Pro	Met Arg Pro Pro Pro	Pro Pro Pro Ala Lys	Ala		
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Pro Asp Pro Gly	His Pro Asp Pro Leu	Thr			
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<210> 316
 <211> 4407
 <212> DNA
 <213> Homo sapiens

<400> 316
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aataaagaac tagcataaca ctcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4350
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4400
aaggaaa 4407

<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

Met Ser Gln Thr Gly Ser His Pro Gly Arg Gly Leu Ala Gly Arg
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Trp Leu Trp Gly Ala Gln Pro Cys Leu Leu Leu Pro Ile Val Pro
20 25 30

Leu Ser Trp Leu Val Trp Leu Leu Leu Leu Leu Leu Ala Ser Leu
35 40 45

Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu
50 55 60

Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser
65 70 75

Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu
80 85 90

Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu
95 100 105

Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly
110 115 120

Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp
125 130 135

Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

	140		145		150
Gly Val Leu Gln Tyr Arg Gly Ala Glu	155	Leu His Leu Gln Pro	160	Leu	165
Glu Gly Gly Thr Pro Asn Ser Ala Gly	170	Gly Pro Gly Ala His	175	Ile	180
Leu Arg Arg Lys Ser Pro Ala Ser Gly	185	Gln Gly Pro Met Cys	190	Asn	195
Val Lys Ala Pro Leu Gly Ser Pro Ser	200	Pro Arg Pro Arg Arg	205	Ala	210
Lys Arg Phe Ala Ser Leu Ser Arg Phe	215	Val Glu Thr Leu Val	220	Val	225
Ala Asp Asp Lys Met Ala Ala Phe His	230	Gly Ala Gly Leu Lys	235	Arg	240
Tyr Leu Leu Thr Val Met Ala Ala Ala	245	Ala Lys Ala Phe Lys	250	His	255
Pro Ser Ile Arg Asn Pro Val Ser Leu	260	Val Val Thr Arg Leu	265	Val	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro	275	Gln Val Gly Pro Ser	280	Ala	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala	290	Trp Gln Arg Gly Leu	295	Asn	300
Thr Pro Glu Asp Ser Gly Pro Asp His	305	Phe Asp Thr Ala Ile	310	Leu	315
Phe Thr Arg Gln Asp Leu Cys Gly Val	320	Ser Thr Cys Asp Thr	325	Leu	330
Gly Met Ala Asp Val Gly Thr Val Cys	335	Asp Pro Ala Arg Ser	340	Cys	345
Ala Ile Val Glu Asp Asp Gly Leu Gln	350	Ser Ala Phe Thr Ala	355	Ala	360
His Glu Leu Gly His Val Phe Asn Met	365	Leu His Asp Asn Ser	370	Lys	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu	380	Ser Thr Ser Arg His	385	Val	390
Met Ala Pro Val Met Ala His Val Asp	395	Pro Glu Glu Pro Trp	400	Ser	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp	410	Phe Leu Asp Asn Gly	415	Tyr	420
Gly His Cys Leu Leu Asp Lys Pro Glu	425	Ala Pro Leu His Leu	430	Pro	435

Val	Thr	Phe	Pro	Gly	Lys	Asp	Tyr	Asp	Ala	Asp	Arg	Gln	Cys	Gln	440	445	450
Leu	Thr	Phe	Gly	Pro	Asp	Ser	Arg	His	Cys	Pro	Gln	Leu	Pro	Pro	455	460	465
Pro	Cys	Ala	Ala	Leu	Trp	Cys	Ser	Gly	His	Leu	Asn	Gly	His	Ala	470	475	480
Met	Cys	Gln	Thr	Lys	His	Ser	Pro	Trp	Ala	Asp	Gly	Thr	Pro	Cys	485	490	495
Gly	Pro	Ala	Gln	Ala	Cys	Met	Gly	Gly	Arg	Cys	Leu	His	Met	Asp	500	505	510
Gln	Leu	Gln	Asp	Phe	Asn	Ile	Pro	Gln	Ala	Gly	Gly	Trp	Gly	Pro	515	520	525
Trp	Gly	Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	530	535	540
Gln	Phe	Ser	Ser	Arg	Asp	Cys	Thr	Arg	Pro	Val	Pro	Arg	Asn	Gly	545	550	555
Gly	Lys	Tyr	Cys	Glu	Gly	Arg	Arg	Thr	Arg	Phe	Arg	Ser	Cys	Asn	560	565	570
Thr	Glu	Asp	Cys	Pro	Thr	Gly	Ser	Ala	Leu	Thr	Phe	Arg	Glu	Glu	575	580	585
Gln	Cys	Ala	Ala	Tyr	Asn	His	Arg	Thr	Asp	Leu	Phe	Lys	Ser	Phe	590	595	600
Pro	Gly	Pro	Met	Asp	Trp	Val	Pro	Arg	Tyr	Thr	Gly	Val	Ala	Pro	605	610	615
Gln	Asp	Gln	Cys	Lys	Leu	Thr	Cys	Gln	Ala	Arg	Ala	Leu	Gly	Tyr	620	625	630
Tyr	Tyr	Val	Leu	Glu	Pro	Arg	Val	Val	Asp	Gly	Thr	Pro	Cys	Ser	635	640	645
Pro	Asp	Ser	Ser	Ser	Val	Cys	Val	Gln	Gly	Arg	Cys	Ile	His	Ala	650	655	660
Gly	Cys	Asp	Arg	Ile	Ile	Gly	Ser	Lys	Lys	Lys	Phe	Asp	Lys	Cys	665	670	675
Met	Val	Cys	Gly	Gly	Asp	Gly	Ser	Gly	Cys	Ser	Lys	Gln	Ser	Gly	680	685	690
Ser	Phe	Arg	Lys	Phe	Arg	Tyr	Gly	Tyr	Asn	Asn	Val	Val	Thr	Ile	695	700	705
Pro	Ala	Gly	Ala	Thr	His	Ile	Leu	Val	Arg	Gln	Gln	Gly	Asn	Pro	710	715	720
Gly	His	Arg	Ser	Ile	Tyr	Leu	Ala	Leu	Lys	Leu	Pro	Asp	Gly	Ser			

	725		730		735									
Tyr	Ala	Leu	Asn	Gly	Glu	Tyr	Thr	Leu	Met	Pro	Ser	Pro	Thr	Asp
				740					745					750
Val	Val	Leu	Pro	Gly	Ala	Val	Ser	Leu	Arg	Tyr	Ser	Gly	Ala	Thr
				755					760					765
Ala	Ala	Ser	Glu	Thr	Leu	Ser	Gly	His	Gly	Pro	Leu	Ala	Gln	Pro
				770					775					780
Leu	Thr	Leu	Gln	Val	Leu	Val	Ala	Gly	Asn	Pro	Gln	Asp	Thr	Arg
				785					790					795
Leu	Arg	Tyr	Ser	Phe	Phe	Val	Pro	Arg	Pro	Thr	Pro	Ser	Thr	Pro
				800					805					810
Arg	Pro	Thr	Pro	Gln	Asp	Trp	Leu	His	Arg	Arg	Ala	Gln	Ile	Leu
				815					820					825
Glu	Ile	Leu	Arg	Arg	Arg	Pro	Trp	Ala	Gly	Arg	Lys			
				830					835					

<210> 318

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 318

ccctgaagct gccagatggc tcc 23

<210> 319

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 319

ctgtgctctt cggatgcagcc agtc 24

<210> 320

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 320
ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 321
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gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100
ctaaatgcag aagcttttta atccaagaaa atatgtaaat cacttaagat 150
ttgtggactg gtgttttgga tcctggccct aactctaatt gtctgtttt 200
gggggagcaa gcacttctgg ccggaggtag ccaaaaaagc ctatgacatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatattcag aagcggaaat ggactgatg 350
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tggttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaa 1197

<210> 322

<211> 317
 <212> PRT
 <213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu	
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Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	
				20					25					30	
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	
				35					40					45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	
				50					55					60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	
				65					70					75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	
				80					85					90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	
				95					100					105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	
				110					115					120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	
				125					130					135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	
				140					145					150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	
				155					160					165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	
				170					175					180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	
				185					190					195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	
				200					205					210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	
				215					220					225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	
				230					235					240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	
				245					250					255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	
				260					265					270	

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
 275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
 290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
 305 310 315

Arg Val

<210> 323
 <211> 1174
 <212> DNA
 <213> Homo sapiens

<400> 323
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 cgttgatcac caccatcctg ccgcaactggc ggaggacagc gcacgtgggc 200
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 ctttagagca caggacaga gggggaaata agaggaggag aaagctctct 1000

ataccaaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050
 atatttatgt ggggtgatttg ataacaagtt taatataaag tgacttggga 1100
 gtttggtcag tggggttggt ttgtgatcca ggaataaacc ttgcggatgt 1150
 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 324
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 Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp
 20 25 30
 Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser
 35 40 45
 Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly
 50 55 60
 Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln
 65 70 75
 Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu
 80 85 90
 Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu
 110 115 120
 Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala
 125 130 135
 Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro
 140 145 150
 Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr
 155 160 165
 Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu
 170 175 180
 Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln
 185 190 195
 Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala
 200 205 210
 Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val
 215 220 225

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
 230 235

<210> 325
 <211> 2121
 <212> DNA
 <213> Homo sapiens

<400> 325
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<210> 326
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 326
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 Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln
 35 40 45
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
 50 55 60
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
 65 70 75
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

80										85					90				
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg					
				95					100					105					
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr					
				110					115					120					
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly					
				125					130					135					
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser					
				140					145					150					
Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val					
				155					160					165					
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val					
				170					175					180					
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala					
				185					190					195					
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser					
				200					205					210					
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe					
				215					220					225					
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile					
				230					235					240					
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro					
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Ser	Lys	His	Asp	Tyr	Val														
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<210> 327
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<400> 327
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 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
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<210> 328
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 328
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 Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn
 35 40 45
 Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile
 50 55 60
 Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
 65 70 75
 Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met
 80 85 90
 Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu
 110 115 120
 Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
 125 130 135
 Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn
 140 145 150
 Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
 155 160 165
 Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala
 170 175 180
 Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
 185 190 195
 Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
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Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
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<210> 329

<211> 1315

<212> DNA

<213> Homo sapiens

<400> 329

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gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
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tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
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Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val
				215					220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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gttccttggc atggtgggga ctcttgccac aacccttctg cctcagtggg 200
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gcaagttcta tagctccttg ttggctctcc cgcttgcctt ggaaacagcc 350
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caagtgtaca atgatggact acttattact ttttgacat catgtattat 1100
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acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

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1	5	10	15
Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg	20	25	30
Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 333
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 ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150
 agaagtatcc agtgggtggc atcccctgcc ccatcacata cctaccagtt 200
 tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
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tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

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Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

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ggcataagtg gaaataaaact caagctgatg cttcaaaaac gagaagcacc 200

tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300

cccgaggtgc agcagtggtg ccagcagttt ctctacatgg gctttgatga 350

agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

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gaagagttaa aacaacacat gtaaatacct ttgatattt catgggaatg 700
cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
<211> 148
<212> PRT
<213> Homo sapiens

<400> 336
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Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
35 40 45
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
50 55 60
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
65 70 75
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
80 85 90
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
95 100 105
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
110 115 120
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
125 130 135
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
140 145

<210> 337
<211> 1310
<212> DNA
<213> Homo sapiens

<400> 337
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gaccactgc ccagccgctc agggacccca acgcatccc agcccagcgc 250

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 cccccagcct gagacacaga ggtcaagctg cacagccaga gccagcacg 350
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 gctacggctg aaattcctca atgattcaga gcagggtggcc agggcctggc 450
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 ctcttgccct ttgcatgta ccgcccgtag tgcctccgcg ggcgcttggc 850
 agcgtcgccg gcccctcccg accttgctcc ccgcgccgcg gcgggagctg 900
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 aaaaaaaaa 1310

<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

Met	Thr	Leu	Ile	Glu	Gly	Val	Gly	Asp	Glu	Val	Thr	Val	Leu	Phe
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Ser	Val	Leu	Ala	Cys	Leu	Leu	Val	Leu	Ala	Leu	Ala	Trp	Val	Ser
				20					25					30
Thr	His	Thr	Ala	Glu	Gly	Gly	Asp	Pro	Leu	Pro	Gln	Pro	Ser	Gly
				35					40					45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	
				50					55					60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	
				65					70					75	
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	
				80					85					90	
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	
				95					100					105	
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	
				110					115					120	
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	
				125					130					135	
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	
				140					145					150	
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	
				155					160					165	
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	
				170					175					180	
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	
				185					190					195	
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
				200					205					210	
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	
				215					220					225	
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	
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Phe	Ala	Met	Tyr	Arg	Pro										
				245											

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

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atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200

tcaggccagc ctcacagtc gctgtgactt ggcccaggtg ctgcagctgg 250

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<210> 340
<211> 148
<212> PRT
<213> Homo sapiens

<400> 340
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Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser
35 40 45
Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser
50 55 60
Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe
65 70 75
Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser
80 85 90
Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn
95 100 105
Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala
110 115 120
Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly
125 130 135
Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg

<210> 341
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 341
 ccctccaagg atgacaaagg cgc 23

<210> 342
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-29
 <223> Synthetic construct.

<400> 342
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<210> 343
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 343
 atctcaggcg gcatcctgtc agcc 24

<210> 344
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 344
 gtggatgcct gcaagaagg tggg 24

<210> 345
 <211> 45
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 345
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<210> 346
<211> 2575
<212> DNA
<213> Homo sapiens

<400> 346
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caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150
aaggagaaaa cgggggtaaa gggagggag caattcaatt tgaagtccct 200
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300
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<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

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Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly	260	265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe			

	545		550		555
Gly Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val					
	560		565		570
Ile Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln					
	575		580		585
His Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser					
	590		595		600
Gly Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu					
	605		610		615
Tyr Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe					
	620		625		630
Asp Gln Ile Asn Ala Val Asp Glu Arg					
	635				

<210> 348
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 348
 ggagaggtgg tggccatgga cag 23

<210> 349
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 349
 ctgtcactgc aaggagccaa cacc 24

<210> 350
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 350
 tatgtcgtg cgaggtgggtg aaaacctoga actgtctttc aaggc 45

<210> 351
<211> 2524
<212> DNA
<213> Homo sapiens

<400> 351
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ccaagcagga ggccaagggg ccggcacagc ccccatccca ctgaggggtgg 1350
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<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

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Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	
				35					40					45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	
				50					55					60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	
				65					70					75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	
				80					85					90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	
				95					100					105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	
				110					115					120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	
				125					130					135	
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
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Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
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Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

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<210> 354
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 354
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 35 40 45
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
 50 55 60
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
 65 70 75
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro
 80 85 90
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
 95 100 105
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
 110 115 120

Ser

<210> 355
 <211> 2134
 <212> DNA
 <213> Homo sapiens

<400> 355
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 tctccaagaa gttctccttc taccgccacc atgtgaactt caagtcctgg 200
 tgggtgggag acatccccgt gtcaggggag ctgctcaccg actggagcga 250
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ctgcgggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356
<211> 157
<212> PRT
<213> Homo sapiens

<400> 356
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20 25 30
Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp
35 40 45
Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr
50 55 60
Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu
65 70 75
Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln
80 85 90
Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu
95 100 105
Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala
110 115 120
Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln
125 130 135
Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

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tcagattcat ctctctctga taatgaacaa ggcctcccca gagtatgaag 550
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ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250
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gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350
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<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

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Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser	20	25	30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	35	40	45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	50	55	60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	65	70	75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	80	85	90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	95	100	105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	110	115	120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	125	130	135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	140	145	150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	155	160	165	
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His	170	175	180	
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	185	190	195	

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 359
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<210> 360
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 360
 tgacgagtgg gatacactgc 20

<210> 361
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 361
 gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
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<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
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<210> 364

<211> 269

<212> PRT

<213> Homo sapiens

<400> 364

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				20					25					30
Leu	Thr	Ala	Gly	Val	Ser	Ala	Leu	Glu	Val	Tyr	Thr	Pro	Lys	Glu
				35					40					45
Ile	Phe	Val	Ala	Asn	Gly	Thr	Gln	Gly	Lys	Leu	Thr	Cys	Lys	Phe
				50					55					60
Lys	Ser	Thr	Ser	Thr	Thr	Gly	Gly	Leu	Thr	Ser	Val	Ser	Trp	Ser
				65					70					75
Phe	Gln	Pro	Glu	Gly	Ala	Asp	Thr	Thr	Val	Ser	Phe	Phe	His	Tyr
				80					85					90
Ser	Gln	Gly	Gln	Val	Tyr	Leu	Gly	Asn	Tyr	Pro	Pro	Phe	Lys	Asp
				95					100					105

Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile
				110					115					120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys
				125					130					135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile
				140					145					150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val
				155					160					165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr
				170					175					180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn
				185					190					195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser
				200					205					210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly
				215					220					225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile
				230					235					240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile
				245					250					255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn	
				260					265					

<210> 365
 <211> 1321
 <212> DNA
 <213> Homo sapiens

<400> 365
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<210> 366
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 366
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 Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg
 20 25 30
 Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly
 35 40 45
 Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu
 50 55 60
 Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu
 65 70 75
 Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro
 80 85 90

Trp	Ser	Pro	Gln	Thr	Pro	Ala	Pro	Pro	Cys	Ser	Arg	Cys	Phe	Ala		95	100	105
Arg	Ala	Ile	Glu	Ser	Ser	Arg	Asp	Leu	Leu	His	Arg	Ile	Lys	Asp		110	115	120
Glu	Val	Gly	Ala	Pro	Gly	Ile	Val	Val	Gly	Val	Ser	Val	Asp	Gly		125	130	135
Lys	Glu	Val	Trp	Ser	Glu	Gly	Leu	Gly	Tyr	Ala	Asp	Val	Glu	Asn		140	145	150
Arg	Val	Pro	Cys	Lys	Pro	Glu	Thr	Val	Met	Arg	Ile	Ala	Ser	Ile		155	160	165
Ser	Lys	Ser	Leu	Thr	Met	Val	Ala	Leu	Ala	Lys	Leu	Trp	Glu	Ala		170	175	180
Gly	Lys	Leu	Asp	Leu	Asp	Ile	Pro	Val	Gln	His	Tyr	Val	Pro	Glu		185	190	195
Phe	Pro	Glu	Lys	Glu	Tyr	Glu	Gly	Glu	Lys	Val	Ser	Val	Thr	Thr		200	205	210
Arg	Leu	Leu	Ile	Ser	His	Leu	Ser	Gly	Ile	Arg	His	Tyr	Glu	Lys		215	220	225
Asp	Ile	Lys	Lys	Val	Lys	Glu	Glu	Lys	Ala	Tyr	Lys	Ala	Leu	Lys		230	235	240
Met	Met	Lys	Glu	Asn	Val	Ala	Phe	Glu	Gln	Glu	Lys	Glu	Gly	Lys		245	250	255
Ser	Asn	Glu	Lys	Asn	Asp	Phe	Thr	Lys	Phe	Lys	Thr	Glu	Gln	Glu		260	265	270
Asn	Glu	Ala	Lys	Cys	Arg	Asn	Ser	Lys	Pro	Gly	Lys	Lys	Lys	Asn		275	280	285
Asp	Phe	Glu	Gln	Gly	Glu	Leu	Tyr	Leu	Arg	Glu	Lys	Phe	Glu	Asn		290	295	300
Ser	Ile	Glu	Ser	Leu	Arg	Leu	Phe	Lys	Asn	Asp	Pro	Leu	Phe	Phe		305	310	315
Lys	Pro	Gly	Ser	Gln	Phe	Leu	Tyr	Ser	Thr	Phe	Gly	Tyr	Thr	Leu		320	325	330
Leu	Ala	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gly	Cys	Lys	Tyr	Leu	Asp		335	340	345
Tyr	Met	Gln	Lys	Ile	Phe	His	Asp	Leu	Asp	Met	Leu	Thr	Thr	Val		350	355	360
Gln	Glu	Glu	Asn	Glu	Pro	Val	Ile	Tyr	Asn	Arg	Ala	Arg				365	370	

<210> 367

<211> 30
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
tggaagagaa gtctgggtcag aaggttttagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
catttggttt cattctctctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
aaaacctcag aacaactcat ttgacacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100
 ctggggcaac cgggctgctc ctgctcttgc tgatggcggt agcagcgccc 150
 agtcgagccc ggggcagcgg ctgccggggc gggactgggt gcgcaggggc 200
 tggggcgga ggtcgagagg gcgaggcctg tggcacgggt gggctgctgc 250
 tggagcactc atttgagatc gatgacagt ccaacttccg gaagcggggc 300
 tcaactgctc ggaaccagca ggatgggtacc ttgtccctgt cacagcgcca 350
 gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400
 gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450
 gaagctgggt gctatgtctc ctcttttgc cctgcgtgct ccctggtgga 500
 gtgcacactg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550
 tgggtggcgt gtcgggtggt acgcaccccg ggggctgccg gggccatgag 600
 gtggaggacg tggacctgga gctgttcaac acctcggtgc agctgcagcc 650
 gccaccaca gcccaggcc ctgagacggc ggccttcatt gagcgcctgg 700
 agatggaaca ggcccagaag gccaagaacc ccaggagca gaagtccttc 750
 ttgcgcaaat actggatgta catcattccc gtctcctgt tcctcatgat 800
 gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850
 gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900
 ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950
 agcttcacgc agccaaaagc aactgttgtt ttggcaagac ggtcctgatg 1000
 tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaacc 1050
 caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100
 ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15
Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
			20						25					30
Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
				35					40					45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	
				50					55					60	
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	
				65					70					75	
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	
				80					85					90	
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	
				95					100					105	
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	
				110					115					120	
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	
				125					130					135	
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	
				140					145					150	
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	
				155					160					165	
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	
				170					175					180	
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	
				185					190					195	
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	
				200					205					210	
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	
				215					220					225	
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	
				230					235					240	
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
				245					250					255	
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
				260					265						

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

ggagcgctgc tggaaccgga gccggagccg gagccacagc ggggaggggtg 50

gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100

cagcaggtcg tccggggggc caccatgctg gtgactgcct accttgcttt 150

tgtaggcctc ctggcctcct gcctgggggt ggaactgtca agatgccggg 200

ctaaaccccc tgggaagggcc tgcagcaatc cctccttcct tcggtttcaa 250
ctggacttct atcaggtcta ctccctggcc ctggcagctg attggcttca 300
ggccccctac ctctataaac totaccagca ttactacttc ctggaaggtc 350
aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450
cctctttctc ctgacttact cactatgctg cttaaccaa ctctctcaag 500
actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550
ctgctcttct cagccttcga ggctggtat atccatgagc acgtggaacg 600
gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650
tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggtgta 700
gccagctgga tagggctggg gcctgtagcg ccctttgtgg ctgccatccc 750
tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800
atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850
ctcctgtcgg accgccgcgt gctgctgctg ggcaccatac aagctctatt 900
tgagagtgtc atcttcatct ttgtcttcct ctggacacct gtgctggacc 950
cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000
ctgcttggct cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050
tcagcccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100
tcttcatggt gactttctct accagcccag gccaggagag tccgggtggag 1150
tccttcatag cctttctact tattgagttg gcttgtggat tatactttcc 1200
cagcatgagc ttcctacgga gaaaggtgat ccctgagaca gagcaggctg 1250
gtgtactcaa ctggttccgg gtacctctgc actcactggc ttgcctaggg 1300
ctccttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatggt 1350
cagcatttgc tctgctgtca tggatgatggc tctgctggca gtggtgggac 1400
tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450
gaggagccct atgccctga gctgtaacct cactccagga caagatagct 1500
gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600
gggaggacat gatgggggtg atggactgga aagaagggtc caaaagttcc 1650

ctctgtgttta ctccatttta gaaaataaac actttttaaat gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser
1 5 10 15

Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly
20 25 30

Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe
35 40 45

Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala
50 55 60

Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly
65 70 75

Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu
80 85 90

Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys
95 100 105

Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu
110 115 120

Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala
125 130 135

Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala
140 145 150

Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu
155 160 165

Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val
170 175 180

Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp
185 190 195

Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu
200 205 210

Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn
215 220 225

Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu
230 235 240

Arg Cys Leu Leu Ser Asp Arg Arg Val	Leu Leu Leu Gly Thr Ile	245	250	255
Gln Ala Leu Phe Glu Ser Val Ile Phe	Ile Phe Val Phe Leu Trp	260	265	270
Thr Pro Val Leu Asp Pro His Gly Ala	Pro Leu Gly Ile Ile Phe	275	280	285
Ser Ser Phe Met Ala Ala Ser Leu Leu	Gly Ser Ser Leu Tyr Arg	290	295	300
Ile Ala Thr Ser Lys Arg Tyr His Leu	Gln Pro Met His Leu Leu	305	310	315
Ser Leu Ala Val Leu Ile Val Val Phe	Ser Leu Phe Met Leu Thr	320	325	330
Phe Ser Thr Ser Pro Gly Gln Glu Ser	Pro Val Glu Ser Phe Ile	335	340	345
Ala Phe Leu Leu Ile Glu Leu Ala Cys	Gly Leu Tyr Phe Pro Ser	350	355	360
Met Ser Phe Leu Arg Arg Lys Val Ile	Pro Glu Thr Glu Gln Ala	365	370	375
Gly Val Leu Asn Trp Phe Arg Val Pro	Leu His Ser Leu Ala Cys	380	385	390
Leu Gly Leu Leu Val Leu His Asp Ser	Asp Arg Lys Thr Gly Thr	395	400	405
Arg Asn Met Phe Ser Ile Cys Ser Ala	Val Met Val Met Ala Leu	410	415	420
Leu Ala Val Val Gly Leu Phe Thr Val	Val Arg His Asp Ala Glu	425	430	435
Leu Arg Val Pro Ser Pro Thr Glu Glu	Pro Tyr Ala Pro Glu Leu	440	445	450

<210> 375
 <211> 1098
 <212> DNA
 <213> Artificial

<400> 375
 gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccgggccccg 50
 gccctggaga tgggtccccgg cgccgcgggc tgggtgttgct tcgtgctctg 100
 gctccccgcg tgcgtgcgcg ccacaggctt ccgtatccat gattatttgt 150
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
 cctgcccaagg actttgggtgg tatctttcac acaaggtatg agcagattca 250

ccttggtcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300
 tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350
 ctctccaaga ctcggtggtt ccaggagcac ggcggggcggg cggatgatcat 400
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
 acagtaacca gcgcacagct gacatccccg ccctcttcct gctcggccga 500
 gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550
 catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600
 tgcaacggcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
 aatttgagga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
 tttgggcgtt gctaggctga aagggaagcc acaccactgg ccttcccttc 800
 cccagggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
 cccaggggtt tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
 gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
 taccagggtt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000
 aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaa 1098

<210> 376
 <211> 188
 <212> PRT
 <213> Homo sapiens

<400> 376
 Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu
 1 5 10 15
 Pro Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu
 20 25 30
 Tyr Phe Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr
 35 40 45
 Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr
 50 55 60
 Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly
 65 70 75
 Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val
 80 85 90

Glu	Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln
				95					100					105
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp
				110					115					120
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg
				125					130					135
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr
				140					145					150
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile
				155					160					165
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu
				170					175					180
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp							
				185										

<210> 377
 <211> 496
 <212> DNA
 <213> Artificial

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50
 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100
 ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctctccta 150
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
 aagaccacagg ggtgcggcat ctacaaggac aacaacaaaa gcagcatata 300
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20						25					30
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35						40					45
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50						55					60
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65						70					75
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80						85					90
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95						100					105
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu				
				110					115					

<210> 379
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 379
 ctgcctccac tgctctgtgc tggg 24

<210> 380
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 380
 cagagcagtg gatgttcccc tggg 24

<210> 381
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt ctttctggat gggggcccag gggggcccagg agagtataaa 50
ggcgtatgtg aggggtgcccg gcacaaccag acgcccagtc acaggcgaga 100
gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150
ctcctggggg gccccacctg ggcaggggaag atgtatggcc ctggaggagg 200
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgga 300
gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400
ctttcctccg gggatatggtc atgtacacca gcaaggaccg ctatttctat 450
tttggggaagc ttgatggcca gatctcctct gcctaccca gccaaagagg 500
gcaggtgctg gtgggcatct atggccagta tcaactcctt ggcatacaaga 550
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600
ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650
ggtatggggc catccgagct gaggccatct gtgtgggtgt ggctgatggt 700
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met	His	Arg	Pro	Glu	Ala	Met	Leu	Leu	Leu	Leu	Thr	Leu	Ala	Leu
1					5				10					15
Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
				20					25					30
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr
				35					40					45

Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln
				50					55					60
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly
				65					70					75
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr
				80					85					90
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met
				95					100					105
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly
				110					115					120
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val
				125					130					135
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly
				140					145					150
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro
				155					160					165
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg		
				170					175					

<210> 384
 <211> 2379
 <212> DNA
 <213> Homo sapiens

<400> 384
 gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50
 agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100
 atacagatgt ggcagctcag gtagcccaa attgcctgga agaatacatc 150
 atgtttttcg ataagaagaa attgtaggat ccagtgtttt ttttaaccgc 200
 cccctcccca cccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250
 atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300
 tgttgggatt tttttgttct tggagtgttc tgcgtggctg gcaaagaata 350
 atgttccaaa atcgggtccat ctccaagggt gtccaatttt tcttcctggg 400
 tgtcagcgag cctgactca ctacagtga gctgacagg gctgtcatgc 450
 aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
 acaaaggatg gggtttcaatg taattaggct actgagcgga tcagctgtag 550
 cactggttat agccccact gtcttactga caatgctttc ttctgccgaa 600
 cgaggatgcc ctaagggtg taggtgtgaa ggcaaatgg tatattgtga 650

atctcagaaa ttacaggaga taccctcaag tataatctgct gggttgcttag 700
 gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750
 aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800
 caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
 ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900
 gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950
 gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000
 ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050
 aacctggaac ttttggacct gggatataac cggatccgaa gtttagccag 1100
 gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
 atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt 1200
 cagaaccttt acttgcaagt gaataaaatc agtgtcatag gacagaccat 1250
 gtccctggacc tggagctcct taaaaaggct tgatttatca ggcaatgaga 1300
 tcgaagcttt cagtggacct agtggtttcc agtgtgtccc gaatctgcag 1350
 cgcctcaacc tggattccaa caagctcaca tttattggtc aagagatttt 1400
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 aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagttttaaa 1500
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 ctacagagag gtttgatctg gccagggctc tcccaaagcc gacgtttaag 1650
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 aaagacagtc cctaaagcaa atgactccca gcacccagga attttatgta 1950
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 ccattgtgat aaaaagagct cttaaaagct gggaaataag tggtgcttta 2100

ttgaactctg gtgactatca aggggaacgcg atgccccccc tccccctccc 2150
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 tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250
 aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300
 ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350
 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385
 <211> 513
 <212> PRT
 <213> Homo sapiens

<400> 385
 Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala
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 Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala
 20 25 30
 Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
 35 40 45
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
 50 55 60
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
 65 70 75
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
 80 85 90
 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
 95 100 105
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
 110 115 120
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
 125 130 135
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
 140 145 150
 Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg
 155 160 165
 Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys
 170 175 180
 Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser
 185 190 195
 Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu

	200	205	210
His Leu Glu His	Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu	Phe
	215	220	225
Pro Arg Leu Val	Ser Leu Gln Asn Leu	Tyr Leu Gln Trp Asn	Lys
	230	235	240
Ile Ser Val Ile	Gly Gln Thr Met Ser	Trp Thr Trp Ser Ser	Leu
	245	250	255
Gln Arg Leu Asp	Leu Ser Gly Asn Glu	Ile Glu Ala Phe Ser	Gly
	260	265	270
Pro Ser Val Phe	Gln Cys Val Pro Asn	Leu Gln Arg Leu Asn	Leu
	275	280	285
Asp Ser Asn Lys	Leu Thr Phe Ile Gly	Gln Glu Ile Leu Asp	Ser
	290	295	300
Trp Ile Ser Leu	Asn Asp Ile Ser Leu	Ala Gly Asn Ile Trp	Glu
	305	310	315
Cys Ser Arg Asn	Ile Cys Ser Leu Val	Asn Trp Leu Lys Ser	Phe
	320	325	330
Lys Gly Leu Arg	Glu Asn Thr Ile Ile	Cys Ala Ser Pro Lys	Glu
	335	340	345
Leu Gln Gly Val	Asn Val Ile Asp Ala	Val Lys Asn Tyr Ser	Ile
	350	355	360
Cys Gly Lys Ser	Thr Thr Glu Arg Phe	Asp Leu Ala Arg Ala	Leu
	365	370	375
Pro Lys Pro Thr	Phe Lys Pro Lys Leu	Pro Arg Pro Lys His	Glu
	380	385	390
Ser Lys Pro Pro	Leu Pro Pro Thr Val	Gly Ala Thr Glu Pro	Gly
	395	400	405
Pro Glu Thr Asp	Ala Asp Ala Glu His	Ile Ser Phe His Lys	Ile
	410	415	420
Ile Ala Gly Ser	Val Ala Leu Phe Leu	Ser Val Leu Val Ile	Leu
	425	430	435
Leu Val Ile Tyr	Val Ser Trp Lys Arg	Tyr Pro Ala Ser Met	Lys
	440	445	450
Gln Leu Gln Gln	Arg Ser Leu Met Arg	Arg His Arg Lys Lys	Lys
	455	460	465
Arg Gln Ser Leu	Lys Gln Met Thr Pro	Ser Thr Gln Glu Phe	Tyr
	470	475	480
Val Asp Tyr Lys	Pro Thr Asn Thr Glu	Thr Ser Glu Met Leu	Leu
	485	490	495

Asn	Gly	Thr	Gly	Pro	Cys	Thr	Tyr	Asn	Lys	Ser	Gly	Ser	Arg	Glu
				500					505					510

Cys Glu Val

<210> 386
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 386
 ctgggatctg aacagtttcg gggc 24

<210> 387
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 387
 ggtccccagg acatggtctg tccc 24

<210> 388
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.

<400> 388
 gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
 <211> 1449
 <212> DNA
 <213> Homo sapiens

<400> 389
 agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
 ttgactgtcc tttaaatatg tcaagatcca gacttttcag tgtcacctca 100
 gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttgggtgct 150
 ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctgggtat atctggatcc tcctgctgct ggtttttggtg 250
 gcagctcttc tctgtggagc tgtgggtcctc tgcctccagt gctggctgag 300
 gagacccoga attgattctc acaggcgcac catggcagtt tttgctgttg 350
 gagacttgga ctctatttat gggacagaag cagctgtgag tccaactgtt 400
 ggaattcacc ttcaaactca aaccctgac ctatatcctg ttctgctcc 450
 atgttttggc cctttaggct cccacctcc atatgaagaa attgtaaaaa 500
 caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
 taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
 tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650
 ggatgttgga aaaaattttg gtcatggaga tgtttaaata gtaaagtagc 700
 aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750
 attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800
 gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850
 tctgctttta actctttcct agcatgggtt ccataaaaat tattataatt 900
 taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950
 agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000
 tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
 gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100
 tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150
 ccaacacggg gagaaaagaa aatttcccct ttacagtaa tgaatgtggc 1200
 ctccatagtc catagtgttt ctctggagcc tcagggttg gcatttattg 1250
 cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300
 gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350
 agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400
 ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
1				5				10					15	

Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
				20					25					30	
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	
			35						40					45	
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu	
			50						55					60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	
			65						70					75	
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	
				80					85					90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
			95						100					105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	
			110						115					120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	
			125						130					135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr					
			140						145						

<210> 391
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 391
 cttttcagtg tcacctcagc gatctc 26

<210> 392
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 392
 ccaaaacatg gagcaggaac agg 23

<210> 393
 <211> 47
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 393
ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 394
gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50
accacccggc gtttctccag ctcgatctgg aggctgcttc gccagtgtgg 100
gacgcagctg acgccoogctt attagctctc gctgcgtcgc cccggctcag 150
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200
tctctttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250
ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggatacaac 300
cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350
ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400
gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
tatgtcccag aaattgagtt tactgttgct tgtatttggg ctcatattggg 500
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550
gtcaagttac gtgagcaaact actagactta agcaaaagat atgttaaagc 600
tctagcagag gaaaataaga acacagtgga tgtcgagaac ggtgcttcta 650
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attttgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750
gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttgggtgc 800
cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850
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tgtacataaa aatttttaaag ttatttgttt gctttcaggc aagtctgttc 1050
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acctttatgt gaagaaatta atttatgcc attgccaggt 2340

<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
1				5				10					15	

Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu
 20 25 30
 His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu
 35 40 45
 Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
 50 55 60
 Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
 65 70 75
 Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu
 80 85 90
 Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
 95 100 105
 Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr
 110 115 120
 Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val
 125 130 135
 Ser Gly Ser Ile Arg
 140

<210> 396
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<400> 396
 cgcgggccggg ccgcccggggg gagcgtgccg aggcggctgt ggcgcaggct 50
 tccagccccc accatgccgt ggcccctgct gctgctgctg gccgtgagtg 100
 gggcccagac aaccgcggcca tgcttccccg ggtgccaatg cgaggtggag 150
 accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200
 cctgggcccc cacatcatgc cggtgcccac ccctctggac acagcccact 250
 tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300
 gggccggggt acacgacgtt ggctggcctg gatctcagcc acaacctgct 350
 caccagcatc tcacccactg cttctctccg ccttcgctac ctggagtgcg 400
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397
 <211> 353
 <212> PRT
 <213> Homo sapiens

<400> 397
 Met Pro Trp Pro Leu Leu Leu Leu Leu Ala Val Ser Gly Ala Gln
 1 5 10 15
 Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr
 20 25 30
 Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser
 35 40 45
 Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
 50 55 60
 Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu
 65 70 75
 Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp
 80 85 90
 Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser
 95 100 105
 Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu
 110 115 120
 Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp
 125 130 135
 Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala
 140 145 150

Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser	155	160	165
His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly	170	175	180
Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg	185	190	195
Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu	200	205	210
Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe	215	220	225
Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln	230	235	240
Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly	245	250	255
Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala	260	265	270
Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp	275	280	285
Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu	290	295	300
His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg	305	310	315
Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly	320	325	330
Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser	335	340	345
Ala Ala Arg Gly Pro Thr Ile Leu	350		

<210> 398
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 398
 ccctgccagc cgagagcttc acc 23

<210> 399
 <211> 23
 <212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgag ccacagcttc tgtgagattc gatttctccc cagttcccct 50

gtgggtctga ggggaccaga agggtagct acgttggtt tctggaagg 100

gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttcccctgaa 150

atgtcattct ctatctattc actgcaagt cctgctgttc caggcottac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaacctt caggaaatac gaaatggatt 500

ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550

gaatcttaag gaggactgag tctttgcaag acacaaagcc tgccaatcga 600

tgctgcctcc tgcgccattt gctaagactc tatctggaca gggatattta 650

aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700

ccaattcctt tcttaccatc aagaaggacc tccggtcttc tcatgccac 750

atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800
 gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850
 gggaaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900
 agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950
 acctgcagag gaggcattgac cccaaaccac catctcttta ctgtactagt 1000
 cttgtgctgg tcacagtgtg tcttatttat gcattacttg cttccttgca 1050
 tgattgtctt tatgcatccc caatcttaat tgagaccata cttgtataag 1100
 atttttgtaa tatctttctg ctattggata tttttattag ttaatatatt 1150
 tttttatttt ttgctattta atgtatttat ttttttactt ggacatgaaa 1200
 ctttaaaaaa attcacagat tatattttata acctgactag agcaggtgat 1250
 gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300
 ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350
 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
 tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450
 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
 aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 402
 Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met
 1 5 10 15
 Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu
 20 25 30
 Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys
 35 40 45
 Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu
 50 55 60
 Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu
 65 70 75
 Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser
 80 85 90

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

<210> 403
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-28
 <223> Synthetic construct.

<400> 403
 ctcctgtggt ctccagattt caggccta 28

<210> 404
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50
aggcttttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggtaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagcttttg caaggagtga 300
caccgcocat ttacagacac gtagtgtatt ctggaggtcg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tccccttttg aaatcagtca ttggagggat gatggctggt gttattggcc 450
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
tgcatttgca aaaatccttag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tggatgaatat ggagattta 650
accacttatg atacagtga acactacttg gtattgaata caccacttga 700
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
gctttttacc atcttggtg agaatgacct cttggtcaat ggtgttctgg 950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala	
				20					25					30	
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr	
				35					40					45	
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp	
				50					55					60	
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala	
				65					70					75	
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly	
				80					85					90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg	
				95					100					105	
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser	
				110					115					120	
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met	
				125					130					135	
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu	
				140					145					150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly	
				155					160					165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile	
				170					175					180	
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro	
				185					190					195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr	
				200					205					210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu	
				215					220					225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu	
				230					235					240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg	
				245					250					255	
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr	
				260					265					270	
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly	
				275					280					285	
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met	
				290					295					300	
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg	

305

310

315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407

<211> 31

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-31

<223> Synthetic construct.

<400> 407

cgcgatccc gttatcgtct tgcgctactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-34

<223> Synthetic construct.

<400> 408

gcggaattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50

tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100

cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150

tagataattt tcgttggcca gaatgtgaat gtattgactg gagtgagaga 200

agaaatgctg tggcatctgt tgcgcaggt atattgtttt ttacaggctg 250

gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300

accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcatg 350

ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400

ctgttttagga agaacagggt ctcgagtttg gcttttcatt ggtttcatgt 450

tgatgtttgg gtcacttatt gcttccatgt ggattctttt tgggtcatat 500

gttaccctaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550

380

tgcacttata ttttttagca ctctgatcta caaatttgga agaaccgaag 600
 agctatggac ctgagatcac ttcttaagtc acattttcct tttgttatat 650
 tctgtttgta gataggtttt ttatctctca gtacacattg ccaaattggag 700
 tagattgtac attaaatggt ttgtttcttt acatttttat gttctgagtt 750
 ttgaaatagt tttatgaaat ttctttattt ttcatgcat agactgttaa 800
 tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850
 tattcctgag atttagaact tgatctactc cctgagccag gggtacatca 900
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 gctcatgcct gtaatcccag cactttggga ggccgaggcg ggccgattgc 1000
 ttgagggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050
 tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100
 cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150
 aggttgcagt gagctgagtt tgcgccactg cactctagcc tgggggagaa 1200
 agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250
 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300
 cataaaaggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350
 ttttttggtg aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400
 tttatataat gattttttta atgcccaaag gactagtttg aaagcttctt 1450
 ttaaaaagaa ttcctcta atgactttat gtgagaa 1487

<210> 410
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 410
 Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys
 1 5 10 15
 Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala
 20 25 30
 Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
 35 40 45
 Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr
 50 55 60
 Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val
 65 70 75

Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu
				80					85					90
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu
				95					100					105
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala
				110					115					120
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe
				125					130					135
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe
				140					145					150
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr							
				155										

<210> 411
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 411
 gtttgaggaa gctgggatac 20

<210> 412
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 412
 ccaaactcga gcacctgttc 20

<210> 413
 <211> 40
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-40
 <223> Synthetic construct.

<400> 413
 atggcaggct tcctagataa ttttcggttg ccagaatgtg 40

<210> 414

<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414
gttgatggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50
gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctggggccc 100
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcatc 350
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500
aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtggggccc 550
tactatgtgc tttgaagacc gcatgatcat gagtccctgtg aaaaacaatg 600
tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750
acgacgatcc agggaccaaa atgaacgatg aaagcaggaa actcttctct 800
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900
taaagaacag cccagacaca aacaaatagc agggatggcc agagctgctg 950
gagatggagg gctgcatgcc cccgaagcca ttttagggtg gctgtggctc 1000
ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050
cccggcaggg gctgaggagg aggagcaggg ggtgctgcgt ggaaggtgct 1100
gcaggtcctt gcacgtgtg tcgcgcctct cctcctcgga aacagaaccc 1150
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200
accagctgtc tgtggagaga atggggtgct ttcgtcaggg actgctgacg 1250
gctggtcctg aggaaggaca aactgccag acttgagccc aattaaattt 1300
tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415
 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
 1 5 10 15
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
 20 25 30
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
 35 40 45
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
 50 55 60
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
 65 70 75
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
 80 85 90
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
 95 100 105
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
 110 115 120
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
 125 130 135
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
 140 145 150
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
 155 160 165
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
 170 175 180
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
 185 190 195
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
 200 205 210
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
 215 220

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-21
<223> Synthetic construct.

<400> 416
gccatagtca cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 418
aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 419
tctgactcct aagtcaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 420
attctctcca cagacagctg gttc 24

<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
tgtctctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
cacgccagga gctcgctcgc tctctctctc tctctctcac tcctccctcc 200
ctctctctct gctgtgctta gtcctctagt cctcaaattc ccagtccctc 250
gcaccccttc ctgggacact atgttgttct ccgccctcct gctggaggtg 300
atttggatcc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaacaatg 400
cccagtogcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
ggacctgcac aacaatggcc acacagtga actctctctg ccctctaccc 550
tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600
cactgggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700
atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900
cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950
gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000
ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050
cagaactacc gagcccttca gcctctcaat cagcgcacatgg tctttgcttc 1100
tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150
gtgtaggaat cttgggtggc tgtctctgcc ttctcctggc tgtttatttc 1200
attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt 1250
cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac 1300
catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350
gggtgtagga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400
ccttcccctg gacatctctt agagaggaat ggacccaggc tgtcattcca 1450
ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500
gaaatcgctg tgttgtaaat gcagaganca aactctgttt agttgcaggg 1550
gaagtttggg atatacccca aagtccctca cccctcact tttatggccc 1600
tttccctaga tatactgcgg gatctctcct taggataaag agttgctggt 1650
gaagttgtat atttttgatc aatatatttg gaaattaaag tttctgactt 1700
t 1701

<210> 423
<211> 337
<212> PRT
<213> Homo sapiens

<400> 423
Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala
1 5 10 15
Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln
20 25 30
Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
35 40 45
Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
50 55 60
Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
65 70 75
Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

80										85					90				
Pro	Ser	Thr	Leu	Tyr	Leu	Gly	Gly	Leu	Pro	Arg	Lys	Tyr	Val	Ala					
				95					100					105					
Ala	Gln	Leu	His	Leu	His	Trp	Gly	Gln	Lys	Gly	Ser	Pro	Gly	Gly					
				110					115					120					
Ser	Glu	His	Gln	Ile	Asn	Ser	Glu	Ala	Thr	Phe	Ala	Glu	Leu	His					
				125					130					135					
Ile	Val	His	Tyr	Asp	Ser	Asp	Ser	Tyr	Asp	Ser	Leu	Ser	Glu	Ala					
				140					145					150					
Ala	Glu	Arg	Pro	Gln	Gly	Leu	Ala	Val	Leu	Gly	Ile	Leu	Ile	Glu					
				155					160					165					
Val	Gly	Glu	Thr	Lys	Asn	Ile	Ala	Tyr	Glu	His	Ile	Leu	Ser	His					
				170					175					180					
Leu	His	Glu	Val	Arg	His	Lys	Asp	Gln	Lys	Thr	Ser	Val	Pro	Pro					
				185					190					195					
Phe	Asn	Leu	Arg	Glu	Leu	Leu	Pro	Lys	Gln	Leu	Gly	Gln	Tyr	Phe					
				200					205					210					
Arg	Tyr	Asn	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Tyr	Gln	Ser	Val					
				215					220					225					
Leu	Trp	Thr	Val	Phe	Tyr	Arg	Arg	Ser	Gln	Ile	Ser	Met	Glu	Gln					
				230					235					240					
Leu	Glu	Lys	Leu	Gln	Gly	Thr	Leu	Phe	Ser	Thr	Glu	Glu	Glu	Pro					
				245					250					255					
Ser	Lys	Leu	Leu	Val	Gln	Asn	Tyr	Arg	Ala	Leu	Gln	Pro	Leu	Asn					
				260					265					270					
Gln	Arg	Met	Val	Phe	Ala	Ser	Phe	Ile	Gln	Ala	Gly	Ser	Ser	Tyr					
				275					280					285					
Thr	Thr	Gly	Glu	Met	Leu	Ser	Leu	Gly	Val	Gly	Ile	Leu	Val	Gly					
				290					295					300					
Cys	Leu	Cys	Leu	Leu	Leu	Ala	Val	Tyr	Phe	Ile	Ala	Arg	Lys	Ile					
				305					310					315					
Arg	Lys	Lys	Arg	Leu	Glu	Asn	Arg	Lys	Ser	Val	Val	Phe	Thr	Ser					
				320					325					330					
Ala	Gln	Ala	Thr	Thr	Glu	Ala													
				335															

<210> 424
 <211> 18
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 424
gtaaagtcgc tggccagc 18

<210> 425
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 425
cccgatctgc ctgctgta 18

<210> 426
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 426
ctgcactgta tggccattat tgtg 24

<210> 427
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 427
cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
aattttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50
acatttttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100
gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150


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aacctgcttt gggactccct ccacaaaaac tggctccgga tcaggaaca 200
ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300
ctgctgcagg aatgacacct ggtaccaga cccaccatt gaccctggga 350
gggttgaatg tacaacagca actgcacca catgtgttac caatttttgt 400
cacacaactt ggagcccagg gactatcct aagctcagag gaattgccac 450
aaatcttcac gagcctcatc atccattcct tgttcccggg aggcacctg 500
cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
agcaggagga gcaggtgtaa atcctgccac ccagggaacc ccagcaggcc 600
gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650
gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaata 700
agcaaataga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750
cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800
gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900
cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950
tatgctgcct ggatgatatg catattaaaa catatttgga aaactggaaa 1000
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
aaaaaaaaaa aaaaaaaaaa aaa 1073

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<210> 429
<211> 209
<212> PRT
<213> Homo sapiens

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<400> 429
Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg
  1             5             10             15

Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys
             20             25             30

Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn
             35             40             45

Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu
             50             55             60

Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met
             65             70             75

```


Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn	80	85	90
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr	95	100	105
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro	110	115	120
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly	125	130	135
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp	140	145	150
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln	155	160	165
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp	170	175	180
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His	185	190	195
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln		200	205	

<210> 430

<211> 1257

<212> DNA

<213> Homo Sapien

<400> 430

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ggagagagggc ggcgcgggtga aaggcgcatt gatgcagcct gcggcggcct 50
cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100
ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
gccccgccgc ctccccgcag cggctccgcg gcctcctgct gctcctgctg 200
ctgcagctgc ccgcgccgtc gagcgctctt gagatcccca aggggaagca 250
aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca 450
actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500
aaaattgcgg agtgtacatt tacaagatg cggtcaaata gtgctctaag 550
agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600
agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650

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attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700
aattaatatt catcgactt cttctgtgga aggactttgt gaaggaattg 750
gtgctggatt agtggatgtt gctatctggg ttggcacttg ttcagattac 800
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900
ttattatgcc ttggaatggg tcacttaaat gacattttta ataatgttat 950
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050
aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100
acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200
aatttgtaaa tgttaagaat tttttttata tctgttaaat aaaaattatt 1250
tccaaca 1257

<210> 431
<211> 243
<212> PRT
<213> Homo Sapien

<400> 431
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
1 5 10 15
Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
20 25 30
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
35 40 45
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

Leu Pro Lys

<210> 432
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial Sequence

<400> 432
 aggacttgcc ctcaggaa 18

<210> 433
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 433
 cgcaggacag ttgtgaaaat a 21

<210> 434
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 434
 atgacgctcg tccaaggcca c 21

<210> 435

<211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 435
 ccacactgta ccacatgt 19

 <210> 436
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 436
 actccaggca ccactgttc tccc 24

 <210> 437
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 437
 aagggtggc attcaagtc 19

 <210> 438
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 438
 tgacctggca aaggaagaa 19

 <210> 439
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 439
 cagccaccct ccagtccaag g 21

 <210> 440
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 440
gggtcgtgtt ttggagaga 19

<210> 441
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 441
ctggccctca gagcaccaat 20

<210> 442
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 442
tcctccatca cttcccctag ctcca 25

<210> 443
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 443
ctggcaggag ttaaagttcc aaga 24

<210> 444
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 444
aaaggacacc gggatgtg 18

<210> 445
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 445
 agcgtacact ctctccaggc aaccag 26

<210> 446
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 446
 caattctgga tgaggtggta ga 22

<210> 447
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 447
 caggactgag cgcttggtta 20

<210> 448
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 <212> DNA
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<220>
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<400> 448
 caaagcgcca agtaccggac c 21

<210> 449
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 449
 ccagacctca gccaggaa 18

<210> 450
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 450
 ccctagctga ccccttca 18

<210> 451
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 451
tctgacaagc agtttttctga atc 23

<210> 452
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 452
ctctccccct cccttttctt ttgttt 26

<210> 453
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 453
ctctggtgcc cacagtga 18

<210> 454
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 454
ccatgcctgc tcagccaaga a 21

<210> 455
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 455
caggaaatct ggaaacctac agt 23

<210> 456
<211> 20
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 456

ccttgaaaag gacccagttt 20

<210> 457

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 457

atgagtgcga cctgctgttc cc 22

<210> 458

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 458

tagcagctgc ccttggtta 18

<210> 459

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 459

aacagcaggt gcgactcatc ta 22

<210> 460

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460

tgctaggcga cgacacccag acc 23

<210> 461

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 461

tggacacgtg gcagtgga 18

<210> 462

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 462

tcatggtctc gtcccatc 19

<210> 463

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 463

caccatttgt ttctctgtct ccccatc 27

<210> 464

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 464

ccggcatcct tggagtag 18

<210> 465

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 465

tccccattag cacaggagta 20

<210> 466

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 466

aggtctttgc ctgtcctgct gct 23

<210> 467

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 467

gcccagagtc ccacttgt 18

<210> 468

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 468

actgctccgc ctactacga 19

<210> 469

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 469

aggcatcctc gccgtcctca 20

<210> 470

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 470

aaggccaagg tgagtccat 19

<210> 471

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 471

cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 472
 tcagggtcta catcagcctc ctgc 24

 <210> 473
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 473
 aaggccaagg tgagtccat 19

 <210> 474
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 474
 cctactgagg agccctatgc 20

 <210> 475
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 475
 tccaggtgga cccacttca gg 22

 <210> 476
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 476
 gggaggctta taggccaat ctgg 24

 <210> 477
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 477

ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50